

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:41:41 : Search time 43.94 Seconds
(without alignments)
90.033 Million cell updates/sec

Title: US-09-825-561A-10
Perfect score: 850
Sequence: 1 MRSSPGNMRITVICMTVFL.....LQKMIHQLSSRTGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 segs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/prodata/2/1aa/ECTUS.COMB.pep: *
6: /cgn2_6/prodata/2/1aa/backfltest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	4	US-09-522-217-2
2	695.5	81.8	519	4	US-09-522-217-85
3	486	57.2	146	4	US-09-522-217-56
4	394	46.4	510	4	US-09-522-217-89
5	212	24.9	40	4	US-09-522-217-72
6	176	20.7	32	4	US-09-522-217-73
7	99.5	11.7	114	1	US-08-031-399-6
8	99.5	11.7	114	1	US-08-031-399-12
9	99.5	11.7	114	1	US-08-393-305-3
10	99.5	11.7	114	1	US-08-726-817-3
11	99.5	11.7	114	1	US-08-504-042-6
12	99.5	11.7	114	1	US-08-504-042-12
13	99.5	11.7	114	2	US-08-725-969-3
14	99.5	11.7	114	2	US-08-725-969-3
15	99.5	11.7	114	4	US-09-189-193-3
16	99.5	11.7	114	5	PCT-US94-03793-6
17	99.5	11.7	114	5	PCT-US94-03793-12
18	99.5	11.7	162	1	US-08-031-399-5
19	99.5	11.7	162	1	US-08-393-305-2
20	99.5	11.7	162	1	US-08-533-733-2
21	99.5	11.7	162	1	US-08-726-817-2
22	99.5	11.7	162	1	US-08-504-042-5
23	99.5	11.7	162	2	US-08-725-969-2
24	99.5	11.7	162	2	US-08-794-524-2
25	99.5	11.7	162	3	US-08-842-947-6
26	99.5	11.7	162	4	US-09-189-193-2
27	99.5	11.7	162	4	US-09-522-217-113

28	99.5	11.7	162	5	PCT-US94-03793-5	Sequence 5, Appl1
29	99.5	11.7	162	5	PCT-US94-06423-2	Sequence 2, Appl1
30	94.5	11.1	114	1	US-08-031-399-3	Sequence 3, Appl1
31	94.5	11.1	114	1	US-08-393-305-6	Sequence 6, Appl1
32	94.5	11.1	114	1	US-08-726-817-6	Sequence 6, Appl1
33	94.5	11.1	114	1	US-08-504-042-3	Sequence 3, Appl1
34	94.5	11.1	114	2	US-08-725-969-6	Sequence 6, Appl1
35	94.5	11.1	114	2	US-08-794-524-6	Sequence 6, Appl1
36	94.5	11.1	114	4	US-09-189-193-6	Sequence 6, Appl1
37	94.5	11.1	114	5	PCT-US94-03793-3	Sequence 3, Appl1
38	94.5	11.1	122	1	US-08-300-903A-3	Sequence 3, Appl1
39	94.5	11.1	162	1	US-08-031-399-2	Sequence 2, Appl1
40	94.5	11.1	162	1	US-08-393-305-5	Sequence 5, Appl1
41	94.5	11.1	162	1	US-08-284-393B-9	Sequence 9, Appl1
42	94.5	11.1	162	1	US-08-726-817-5	Sequence 5, Appl1
43	94.5	11.1	162	1	US-08-504-042-2	Sequence 2, Appl1
44	94.5	11.1	162	2	US-08-725-969-5	Sequence 5, Appl1
45	94.5	11.1	162	2	US-08-794-524-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-522-217-2
Sequence 2, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-2

Query Match 100.0% Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.8e-87;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMRITVICMTVFLGLTVHKSSSGGODRHMRMQLIDYDQKNTYNDLVPF 60
DB 1 MRSSPGNMRITVICMTVFLGLTVHKSSSGGODRHMRMQLIDYDQKNTYNDLVPF 60
QY 61 LAPEDVEFNCSWAFSCFOKAOLKSANTGNENIIVASTIKLKKRPPTNAGRQKHNL 120
DB 61 LAPEDVEFNCSWAFSCFOKAOLKSANTGNENIIVASTIKLKKRPPTNAGRQKHNL 120
QY 121 TPCSDSYEKKKPEFLERFKSLQKMIHQLSSRTGSEDS 162
DB 121 TPCSDSYEKKKPEFLERFKSLQKMIHQLSSRTGSEDS 162

RESULT 2

US-09-522-217-85

Sequence 85, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

EARLIER FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 85

LENGTH: 519

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide

US-09-522-217-85

Query Match

Best Local Similarity 81.8%; Score 695.5; DB 4; Length 519;

Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Db 23 LVHSSSGODRRHIMRQLIDIVDLKNVNDLVPFLPAPEDEVETNCENSAFSCFOKA 82

Db 383 LVRGSG--QDRHIMRQLIDIVDLKNVNDLVPFLPAPEDEVETNCENSAFSCFOKA 439

QY 83 QLSANTGNERTINVSITKIKRPPSTNAGRQKHRLTSCSCSYEKRPKEFLERFKS 142

Db 440 QLSANTGNERTINVSITKIKRPPSTNAGRQKHRLTSCSCSYEKRPKEFLERFKS 499

Db 143 LQKMIHQLSRKTHGSEDS 162

Db 500 LQKMIHQLSRKTHGSEDS 519

RESULT 3

US-09-522-217-56

Sequence 56, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

Query Match

Best Local Similarity 46.4%; Score 394; DB 4; Length 510;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

Db 33 DRHIMRQLIDIVDLKNVNDLVPFLPAPEDEVETNCENSAFSCFOKAQLSANTGN 92

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 56

LENGTH: 146

TYPE: PRT

ORGANISM: mus musculus

US-09-522-217-56

Query Match

Best Local Similarity 57.2%; Score 486; DB 4; Length 146;

Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVCIAMVFLCTLVHSSSGODRRHIMRQLIDIVDLKNVNDLVPFLPAPEDEV 67

Db 1 MERIVCIAMVFLCTLVHSSSGODRRHIMRQLIDIVDLKNVNDLVPFLPAPEDEV 60

QY 68 ETNCENSAFSCFOKAQLSANTGNERTINVSITKIKRPPSTNAGRQKHRLTSCSCDS 127

Db 61 KGHCHAAFAFCFOKAKLPSNPNKTFITDLVAQLRRLPARGQKQKHIAKCPSCDS 120

QY 128 YEKRPKEFLERFKSILQKMIHQLS 153

Db 121 YEKRPKEFLERFKSILQKMIHQLS 146

RESULT 4

US-09-522-217-89

Sequence 89, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

EARLIER FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: MBP-mouse zalpha11 ligand fusion polypeptide

US-09-522-217-89

Query Match

Best Local Similarity 46.4%; Score 394; DB 4; Length 510;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

Db 33 DRHIMRQLIDIVDLKNVNDLVPFLPAPEDEVETNCENSAFSCFOKAQLSANTGN 92

Fri Jun 28 07:58:54 2002

us-09-825-561a-10.raii

Page 4

[illegible]

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      RESULT      8
US-08-031-399-12
      : Sequence 12, Application US/08031399
      : Patent No. 5552303
      :
      : GENERAL INFORMATION:
      :
      : APPLICANT: Grabstein, Kenneth
      :
      : APPLICANT: Anderson, Dirk
      :
      : APPLICANT: Eisenman, June
      :
      : APPLICANT: Fung, Victor
      :
      : APPLICANT: Rauch, Charles
      :
      : TITLE OF INVENTION: Epithelium-derived T-cell Factor
      :
      : NUMBER OF SEQUENCES: 12
      :
      : CORRESPONDENCE ADDRESS:
      :
      : ADDRESSEE: Immunex Corporation
      :
      : STREET: 51 University Street
      :
      : CITY: Seattle
      :
      : STATE: Washington
      :
      : COUNTRY: USA
      :
      : ZIP: 98101
      :
      : COMPUTER READABLE FORM:
      :
      : MEDIUM TYPE: Floppy disk
      :
      : COMPUTER: IBM PC compatible
      :
      : OPERATING SYSTEM: PC-DOS/MS-DOS
      :
      : SOFTWARE: Patentia Release #1.0, Version #1.25
      :
      : CURRENT APPLICATION DATA:
      :
      : APPLICATION NUMBER: US/08/031,399
      :
      : FILING DATE: 19930308
      :
      : CLASSIFICATION: 530
      :
      : ATTORNEY/AGENT INFORMATION:
      :
      : NAME: Launer, Charlene
      :
      : REGISTRATION NUMBER: 33,035
      :
      : REFERENCE/DOCKET NUMBER: 2811
      :
      : TELECOMMUNICATION INFORMATION:
      :
      : TELEPHONE: 206-587-0430
      :
      : INFORMATION FOR SEQ ID NO: 12:
      :
      : SEQUENCE CHARACTERISTICS:
      :
      : LENGTH: 114 amino acids
      :
      : TYPE: AMINO ACID
      :
      : TOPOLOGY: linear
      :
      : MOLECULE TYPE: protein
      :
      : HYPOTHEICAL: NO
US-08-031-399-12

```

```

Query Match Score 99.5% DB 1: Length 114:
Best Local Similarity 25.28; Pred. No. 0.0086;
Matches 30; Conservative 23; Mismatches 45; Indels 21; Gaps 5

QY      43 IDIVDOLKANYNDLVPPE-----LPAPEDVETNCESMSHSCF-QKQDLKSANTGNN---- 92
       :::: | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      3 VNVISLAK-IEDLIOSMHDATLYTESVHNSCKAYAMCFLEIQLQVITSNMSGPXIHID 61
QY      93 --ERIINVSIRKLKRPPSTNAGROKHRLTGPCSDCYEKPKPFELERFKSLQKKMH 149
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      62 IVENILLILANXXLSNGNXTESG-----CKKEEFLERKNIKRFLQSFVAHYQMFIN 112

RESULT          9
US-08-393-305-3
: sequence 3, Application US/08393305
```

```

Patent No. 5574138
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,305
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
us-08-393-305-3

Query Match 11.7%; Score 99.5; DB 1; Length 114;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

0Y 43 IDVDLTKYVNDIVPEF-----LPAPEDVETNCEMSAFSCF-----QKMKLSANTGNNE 93
   ::: ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 3 VNVISDIKK-IEDLIQSMHIDALVLTESDVHRSCKVYNAKCFLEELQVLSLESDASHTD 61
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

0Y 94 RIINVSIRKKLRKPPSTINAGROKKNHLICPSDSDEYKKPKPEFLERFKSLQKMH 149
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 62 IYENLIT--LANNSSISNGVATSS--GKRCDELEERKNTKEFLQSFVHIYVDFPIN 112
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

```

RESULT 10
 US-08-726-817-3
 : Sequence 3, Application US/08726817
 : Patent No. 5707616
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Gradstein, Kenneth
 : APPLICANT: Anderson, Dirk
 : APPLICANT: Eisenman, June
 : APPLICANT: Fung, Victor
 : APPLICANT: Rauch, Charles
 : TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
 :
 : NUMBER OF SEQUENCES: 15
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Seed and Berry
 : STREET: 6500 Columbia Center, 701 Fifth Avenue
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: USA
 :
 : ZIP: 98104
 :
 : COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-817-3

Query Match 11.7%; Score 99.5; DB 1; Length 114;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVOLKKNVNDVPER-----LPAPDEVETNCWMSAFSCF-----OKAOLKSANTGNNE 93
DB 3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCVTAMKCFLLLEQVLSLSDGASIH 61
OY 94 RIIVSIRKIKRPPSTNAGRQKHRLTSPSCDSYERKPKPEFLERFKSLQKMH 149
DB 62 TVENLI--LANNSSLSSNGVTES---GCKECELEEKNIKEFLQSFVHIQWFTN 112

RESULT 11
US-08-504-042-6
Sequence 6, Application US/08504042
Patent No. 5747024
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,399
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-504-042-6

Query Match 11.7%; Score 99.5; DB 1; Length 114;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVOLKKNVNDVPER-----LPAPDEVETNCWMSAFSCF-----OKAOLKSANTGNNE 93
DB 3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCVTAMKCFLLLEQVLSLSDGASIH 61
OY 94 RIIVSIRKIKRPPSTNAGRQKHRLTSPSCDSYERKPKPEFLERFKSLQKMH 149
DB 62 TVENLI--LANNSSLSSNGVTES---GCKECELEEKNIKEFLQSFVHIQWFTN 112

RESULT 12
US-08-504-042-12
Sequence 12, Application US/08504042
Patent No. 5747024
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,399
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-504-042-12

RESULT 14

RESULT 15

ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue

```

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMAsters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-189-193-3

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	Query Match	Similarity	Score	DB 4	Length
Best Local	30	Conservative	25.9%	Pred. No. 0.00086	114
Matches	30	Conservative	23	Mismatches	46
				Indels	15
				Gaps	5
Oy	43	IDIYQVLKNYVDLPDEF-----LPAPEDVEVNCMSAFSCF-----OKAQLKSANTGNNE	93		
Db	3	VNVISDLKK-IEDLLQSMHIDATLYTTESDYPHSCVYTKMCKLLEIQVLSLESGASHND	61		
Oy	94	RIINSIKKKRPPSTNAGRQKRLHLCPCSDSEYKPKPFELREFKSLLOKMT	149		
Db	62	TVENLIT-LANNSLSSNGVTES---GCKEEELLEKIKIRFLOSFVAIVGMFIN	112		

Search completed: June 28, 2002, 07:41:41
Job time: 56 sec

GenCore Version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:41:39 ; Search time 43.94 Seconds
(Without alignments)

121.183 Million cell updates/sec

Title: US-09-825-561A-6

Sequence: 1 CPDLCYDYDQVTCILEM.....SDPVLEQOQSEELKEGWNPH 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	538	3 US-09-040-005-2	Sequence 2, Appl
2	1195	100.0	538	4 US-09-522-217-115	Sequence 115, Appl
3	1195	100.0	606	4 US-09-522-217-97	Sequence 97, Appl
4	144	12.1	894	2 US-08-599-455B-2	Sequence 2, Appl
5	144	12.1	894	4 US-09-069-781B-2	Sequence 2, Appl
6	144	12.1	894	4 US-08-618-957A-12	Sequence 12, Appl
7	144	12.1	1162	2 US-08-599-455B-43	Sequence 43, Appl
8	144	12.1	1162	4 US-09-069-781B-12	Sequence 12, Appl
9	142.5	11.9	896	2 US-08-640-389A-12	Sequence 12, Appl
10	141.5	11.8	539	6 5198359-4	Patent No. 5198359
11	141.5	11.8	539	6 5449756-4	Patent No. 5449756
12	139	11.6	493	2 US-08-078-311-7	Sequence 7, Appl
13	139	11.6	493	2 US-08-460-402-7	Sequence 7, Appl
14	139	11.6	635	1 US-08-184-327A-4	Sequence 4, Appl
15	139	11.6	635	2 US-08-078-311-1	Sequence 1, Appl
16	139	11.6	635	2 US-08-460-402-1	Sequence 1, Appl
17	139	11.6	635	5 PCT-US95-00670-4	Sequence 4, Appl
18	138	11.5	895	4 US-08-827-962-19	Sequence 19, Appl
19	138	11.5	1162	4 US-08-827-962-15	Sequence 15, Appl
20	138	11.5	1162	4 US-08-803-346-1	Sequence 1, Appl
21	137	11.5	1165	2 US-08-589-455B-4	Sequence 4, Appl
22	137	11.5	1165	4 US-09-093-814-1	Sequence 1, Appl
23	137	11.5	1165	4 US-09-069-781B-4	Sequence 4, Appl
24	137	11.5	1165	4 US-08-618-957A-11	Sequence 11, Appl
25	136	11.4	569	1 US-08-306-231-3	Sequence 3, Appl
26	136	11.4	896	4 US-08-618-957A-10	Sequence 10, Appl
27	136	11.4	898	2 US-08-693-697-36	Sequence 36, Appl

ALIGNMENTS

28	136	11.4	906	4 US-08-618-957A-9	Sequence 9, Appl
29	136	11.4	908	2 US-08-693-697-33	Sequence 33, Appl
30	136	11.4	908	2 US-08-588-526-3	Sequence 3, Appl
31	136	11.4	958	4 US-08-618-957A-8	Sequence 8, Appl
32	136	11.4	960	1 US-08-355-888A-8	Sequence 8, Appl
33	136	11.4	960	2 US-08-588-190-3	Sequence 3, Appl
34	136	11.4	960	2 US-08-693-697-8	Sequence 8, Appl
35	136	11.4	960	2 US-08-618-957A-3	Sequence 3, Appl
36	136	11.4	960	2 US-08-693-697-3	Sequence 3, Appl
37	136	11.4	960	4 US-08-618-957A-3	Sequence 3, Appl
38	135	11.3	1162	4 US-08-827-962-20	Sequence 20, Appl
39	133.5	11.2	369	2 US-08-424-224-2	Sequence 2, Appl
40	133.5	11.2	369	5 PCT-US94-02891-69	Sequence 69, Appl
41	133.5	11.1	382	2 US-08-078-311-3	Sequence 3, Appl
42	133.5	11.1	382	2 US-08-460-402-3	Sequence 3, Appl
43	132.5	11.1	482	1 US-08-184-327A-8	Sequence 8, Appl
44	132.5	11.1	482	5 PCT-US95-00670-8	Sequence 8, Appl
45	132.5	11.1	626	1 US-08-184-327A-2	Sequence 2, Appl

RESULT 1
US-09-040-005-2
; Sequence 2, Application US/09040005
; Patent No. 6057128
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; TITLE OF INVENTION: Unger, Michelle
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; STREET: 87 Cambridge Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,005
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A 32,724
; REGISTRATION NUMBER: G15320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-040-005-2
Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.1e-123; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0;
QY 1 CPDLCYDYDQVTCILEMNLHPSTLTLTQDOYELKDEATSCSLHRSANATHATY 60
DB 20 CPDLCYDYDQVTCILEMNLHPSTLTLTQDOYELKDEATSCSLHRSANATHATY 79

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QY 61 TCHMDVHFHMADDIFSVNTTDSGNVSOBCGSFLLAESIKRPAPEPNVTVTSGOYNISM 120
      |||
Db 80 TCHMDVHFHMADDIFSVNTTDSGNVSOBCGSFLLAESIKRPAPEPNVTVTSGOYNISM 139
QY 121 SDYEDAFYMLKGKLOYELQYRNKRGDPMAVSPRRKLISVDSRSVSLPLFERKDSYELQ 180
      |||
Db 140 SDYEDAFYMLKGKLOYELQYRNKRGDPMAVSPRRKLISVDSRSVSLPLFERKDSYELQ 199
QY 181 VRAGPMPGSSYOGTWSWSDPVIPTQOSEELKEGWNPH 218
      |||
Db 200 VRAGPMPGSSYOGTWSWSDPVIPTQOSEELKEGWNPH 237
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RESULT 2
US-09-522-217-115
; Sequence 115, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115
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Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CPDLVCTYTYLQTVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSANHTATY 60
|||
Db 20 CPDLVCTYTYLQTVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSANHTATY 79
QY 61 TCHMDVHFHMADDIFSVNTTDSGNVSOBCGSFLLAESIKRPAPEPNVTVTSGOYNISM 120
|||
Db 80 TCHMDVHFHMADDIFSVNTTDSGNVSOBCGSFLLAESIKRPAPEPNVTVTSGOYNISM 139
QY 121 SDYEDAFYMLKGKLOYELQYRNKRGDPMAVSPRRKLISVDSRSVSLPLFERKDSYELQ 180
|||
Db 140 SDYEDAFYMLKGKLOYELQYRNKRGDPMAVSPRRKLISVDSRSVSLPLFERKDSYELQ 199
QY 181 VRAGPMPGSSYOGTWSWSDPVIPTQOSEELKEGWNPH 218
|||
Db 200 VRAGPMPGSSYOGTWSWSDPVIPTQOSEELKEGWNPH 237
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RESULT 3
US-09-522-217-97
; Sequence 97, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
```

```
; APPLICANT: No. 6307024a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphan1 soluble receptor polypeptide sequence
US-09-522-217-97
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Query Match 100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CPDLVCTYTYLQTVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSANHTATY 60
|||
Db 389 CPDLVCTYTYLQTVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSANHTATY 448
QY 61 TCHMDVHFHMADDIFSVNTTDSGNVSOBCGSFLLAESIKRPAPEPNVTVTSGOYNISM 120
|||
Db 449 TCHMDVHFHMADDIFSVNTTDSGNVSOBCGSFLLAESIKRPAPEPNVTVTSGOYNISM 508
QY 121 SDYEDAFYMLKGKLOYELQYRNKRGDPMAVSPRRKLISVDSRSVSLPLFERKDSYELQ 180
|||
Db 509 SDYEDAFYMLKGKLOYELQYRNKRGDPMAVSPRRKLISVDSRSVSLPLFERKDSYELQ 568
QY 181 VRAGPMPGSSYOGTWSWSDPVIPTQOSEELKEGWNPH 218
|||
Db 569 VRAGPMPGSSYOGTWSWSDPVIPTQOSEELKEGWNPH 606
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RESULT 4
US-08-599-455B-2
; Sequence 2, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
```


APPLICANT: Smodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pastco Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-618-957A-12

Query Match	12.1%;	Score 144;	DB 4;	Length 894;
Best Local Similarity	31.1%;	Pred. No. 4.4e-07;		
Matches 57;	Conservative 22;	Mismatches 60;	Indels 44;	Gaps 11

[illegible]

RESULT 7
US-08-599-455B-43
; Sequence 43, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.

```

1  APPLICATION: Culpepper, Janice A.
2  TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
3  TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
4  NUMBER OF SEQUENCES: 44
5  CORRESPONDENCE ADDRESS:
6  ADDRESSER: Fish & Richardson, P.C.
7  STREET: 225 Franklin Street
8  CITY: Boston
9  STATE: MA
10 COUNTRY: US
11 ZIP: 02110-2804
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM Compatible
15 OPERATING SYSTEM: Windows95
16 SOFTWARE: FASTSEQ for Windows Version 2.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/599,455B
19 FILING DATE: 22-JAN-1996
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 08/583,153
22 FILING DATE: 28-DEC-1995
23 APPLICATION NUMBER: 08/570,142
24 FILING DATE: 11-DEC-1995
25 APPLICATION NUMBER: 08/569,485
26 FILING DATE: 08-DEC-1995
27 APPLICATION NUMBER: 08/566,622
28 FILING DATE: 04-DEC-1995
29 APPLICATION NUMBER: 08/562,663
30 FILING DATE: 27-NOV-1995
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Melkielejoh, Ph.D., Anita L.
33 REGISTRATION NUMBER: 35,283
34 REFERENCE/DOCKET NUMBER: 07334/017001
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 617-542-5070
37 TELEFAX: 617-542-8906
38 TELEX: 200154
39 INFORMATION FOR SEQ ID NO: 43:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 1162 amino acids
42 TYPE: amino acid
43 TOPOLOGY: linear
44 MOLECULE TYPE: protein
45 FRAGMENT TYPE: internal
46 US-08-599-455B-43 Internal

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Query Match 12.1%; Score 144; DB 2; Length 1162;
Best Local Similarity 31.1%; Pred. No. 6.5e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11.

QY	39	IKDE-----	ATGSLRHSANMNT	HAATYTC	CHNDYH-----	PAADITSVNT	QSGNYS	87
Db	177	LKSFQTVQ	QNCNSL	KGC-----	EC	HPVPRAKI	NALMLY	ETISAGVS
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QY	88	QEGSGE	SLLAESIK	PAP--	FNVTV	FSGONIS	WRSDY	EDDPAFYMLK
Db	228	LQ--	PMIV--	VKPP	PIGLHME	YTDG	GNLKIS	WDSQ
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QY	146	DPM	AVSPRR	KLISV	SRSY--	SLLE	PLFRK	QSSYELQYR
Db	277	T--	IVREAE	IVSATS	LLYD	SLP-----	GSSYE	VOVRSKR
								326
QY	205	QTQ	207					
Db	327	TTQ	329					

RESULT 8
US-09-069-781B-43
; Sequence 43, Application US/09069781B
; Patent No. 6287782


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GENERAL INFORMATION:
APPLICANT: Tarcaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkiesohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-09-069-781B-43

Query Match 12.1%; Score 144; DB 4; Length 1162;
Best Local Similarity 31.1%; Pred. No. 6.5e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATGCSLHSAHNAHTATYCHMDVPH-----FMADDIFSVNITDQSGNTS 87
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DB 177 LKDSQFOVQCNCLRG-----ECHVVPRAKINVALMLYLETTSAGVSFQSPILMS 227

QY 86 ORCGSGFLAESTKPAAP--FNVVTYFSGOVNISWRSDYEDPAFYMLKGLQYELQYRRGDPMAVSPRRKL 145
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 228 LQ--PMLV---VKDPPLGLHMEVTDGNNLKISWDSOTMAF-----PLQYQVYKL--ENSTIYREAXEL 276

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QY 146 DPMAVSPRRKLISVDSRSV-SLLPLFRKDSYELQYRAGPMGSSYQGTWSEWSPVIF 204
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DB 277 T--TYREAELVTSATSLVDVLP-----GSSYEVQYRSRLDGS---GWSMDSSPDVF 326

QY 205 QYQ 207
  ||
DB 327 TTQ 329

RESULT 9
US-08-640-389A-12
Sequence 12, Application US/08640389A
Patent No. 5912123
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Clouff, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEPTIN
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-640-389A-12

Query Match 11.9%; Score 142.5; DB 2; Length 896;
Best Local Similarity 28.4%; Pred. No. 6.5e-07;
Matches 66; Conservative 29; Mismatches 82; Indels 55; Gaps 14;

QY 3 DLVCY-TDYLQVYICLLEWNLHP-----STLTLLTW-----ODQYEELKDE---ATS 45
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 128 DICWKKGDKLFCIMHEPLPKNPKNDKSKVHLIYDLPEVIDSPILPKDSQFOVQCN 187

QY 46 CSLSHSAHNAHTATYCHMDVPH-----FMADDIFSVNITDQSGVSOECGSLAAS 98
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 188 CSL-----RCXKCHVVPRAKINVALMLYLETTSAGVSFQSPILMSLQ--PMLV--- 234

QY 99 IKPAPP--FNVVTYFSGOVNISWRSDYEDPAFYMLKGLQYELQYRRGDPMAVSPRRKL 156
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 235 VKDPPLGLHMEVTDGNNLKISWDSOTMAF-----PLQYQVYKL--ENSTIYREAXEL 287

QY 157 ISVDSRSV-SLLPLFRKDSYELQYRAGPMGSSYQGTWSEWSPVIFOTQ 207

```

Db 288 VSATISLTVSLVDP-----GSSYEVQVRKRLDGS---GWSMDSSPOVFTTQ 331

RESULT 10

5198359-4

APPLICANT: TANIGUCHI, TADATSUGU; JATAKEYAMA, MASANORI;
MINAMOTO, SEIICHI; KONO, TAKESHI; DOI, TAKESHI; MITASAKA, MASAYUKI;
TSUDO, MITSURU; KASUYAMA, HAJIME

TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,059

FILING DATE: 05-MAR-1990

SEQ ID NO: 4

LENGTH: 539

5198359-4

Query Match

11.8%; Score 141.5; DB 6; Length 539;

Best Local Similarity 22.5%; Pred. No. 4e-07;

Matches 54; Conservative 43; Mismatches 86; Indels 57; Gaps 12;

1 CPDVCYTDVLTQVLCILEMWNLPSTLTFTWQDYEELKDEATSCSLRSANHTATY 60

31 CSHLECFYNSRANVSC---MMS-HEBALNV-----TTCHVHAKS-NLRHWK 72

61 TCHMDVFN-----FMADIFSVNIT--DQSGNYSQEGCSFLLAESIK 100

73 TCELTIVRQASMACNLILGSPESQSLTSVDLIDINVCMEKGRVKTCDFFHPFNLR 132

101 PAPFNVTYTF--SGQYNISM---SDYEDPAFYMLKGLQYELQYRNRPAAVSPPR 154

133 LVAPHSLQVLIHDITQRCNISMKVSOVSHYIEP-----YLEFEARRRLGHSMEDA--- 182

155 KLISVDSRSVSLPLFPRKDSYELQVRAGPMPGSSYGTGSEMSDPYIFQTO--SEELKE 213

183 SVLSLKRQOQWLFLEMLIPSTSYEVQVRKARNNT--GTWSPMSQPLTFRTPRADPKE 240

RESULT 11

5449756-4

APPLICANT: TANIGUCHI, TADATSUGU; HATAKEYAMA, MASANORI; MINAMOTO,
SEIICHI; KONO, TAKESHI; DOI, TAKESHI; MITASAKA, MASAYUKI; TSUDO,
MITSURU; KASUYAMA, HAJIME

TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/88,592

FILING DATE: 9-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 865,155

FILING DATE: 08-APR-1992

APPLICATION NUMBER: 487,059

FILING DATE: 05-MAR-1990

SEQ ID NO: 4

LENGTH: 539

5449756-4

Query Match

11.8%; Score 141.5; DB 6; Length 539;

Best Local Similarity 22.5%; Pred. No. 4e-07;

Matches 54; Conservative 43; Mismatches 86; Indels 57; Gaps 12;

1 CPDVCYTDVLTQVLCILEMWNLPSTLTFTWQDYEELKDEATSCSLRSANHTATY 60

31 CSHLECFYNSRANVSC---MMS-HEBALNV-----TTCHVHAKS-NLRHWK 72

61 TCHMDVFN-----FMADIFSVNIT--DQSGNYSQEGCSFLLAESIK 100

73 TCELTIVRQASMACNLILGSPESQSLTSVDLIDINVCMEKGRVKTCDFFHPFNLR 132

QY 101 PAPFNVTYTF--SGQYNISM---SDYEDPAFYMLKGLQYELQYRNRPAAVSPPR 154

DB 133 LVAPHSLQVLIHDITQRCNISMKVSOVSHYIEP-----YLEFEARRRLGHSMEDA--- 182

QY 155 KLISVDSRSVSLPLFPRKDSYELQVRAGPMPGSSYGTGSEMSDPYIFQTO--SEELKE 213

DB 183 SVLSLKRQOQWLFLEMLIPSTSYEVQVRKARNNT--GTWSPMSQPLTFRTPRADPKE 240

RESULT 12

US-08-078-311-7

Sequence 7, Application US/08078311

Patent No. 5925750

GENERAL INFORMATION:

APPLICANT: Charon, Martine

APPLICANT: Gisselbrecht, Sylvie

APPLICANT: Penciolelli, Jean-Francois

APPLICANT: Souyri, Michele

APPLICANT: Tambourin, Pierre

APPLICANT: Varlet, Paule

APPLICANT: Vigon, Isabelle

APPLICANT: Wendling, Francoise

TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor

TITLE OF INVENTION: Family Application in the Diagnosis and Treatment of

MYELOPROLIFERATIVE DISEASE

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 3100 No. 5925750west Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/078,311

FILING DATE: 18-JUN-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/FR90/00762

FILING DATE: 19-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Kowalchuk, Katherine M.

REGISTRATION NUMBER: 36,848

REFERENCE/DOCKET NUMBER: 8076.84USMO

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 493 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-078-311-7

Query Match 11.6%; Score 139; DB 2; Length 493;

Best Local Similarity 24.0%; Pred. No. 6.6e-07;

Matches 59; Conservative 25; Mismatches 76; Indels 86; Gaps 14;

QY 4 LVCTDVLQVLCILEMWNLPSTLTFTWQDYEELKDEATSCSL--HRSANHTATY- 60

DB 289 LQCFPLDKNVTG-----QWQOQ-----DHASQGFYSRRARCCPRPRYP 329

QY 61 -----TCHM-----DVHFMAADIFSVNITDQSGNYSQEGCS-F 93

DB 330 IWENCEBEKNTPLQTPQFSRCHFRKSRNDSITIHIL-----VEVTTAPGTVHSLGSPF 383

Db 330 IWENCEEETKNTNPGLOTPQFSRCHFKSRNDSIIHL-----VEYTTAPGVHSTYLSPE 383
QY 94 LLAESIK-PAPPEENVTVTFESGOYNISWRSDYEDPAFYMLKGKIQYELQYRNNG-DPWAVS 151
Db 384 WTHQAVRLPTNLMHREISSGHLEW---QHPSSMAQ-ETCYQLRTYGEHGMKV- 437
QY 152 PRKRLISVDSRSVSLP-----LEFRKDSYELQYRAGPMPGSSYQGTWSEWSDPVI 203
Db 438 -----LEPPLGARGTLELRPRSRVRLQLR-RLNGPTYQGPWSSWSDPTR 482
QY 204 FOTQSE 209
Db 483 VETATE 488

RESULT 15
US-08-078-311-1
; Sequence 1, Application US/08078311
; Patent No. 5925750
; GENERAL INFORMATION:
; APPLICANT: Charon, Martine
; APPLICANT: Gisselbrecht, Sylvie
; APPLICANT: Penciolelli, Jean-Francis
; APPLICANT: Souyil, Michele
; APPLICANT: Tambourin, Pierre
; APPLICANT: Varlet, Paule
; APPLICANT: Vigon, Isabelle
; TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
; TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5925750west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,311
; FILING DATE: 18-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NO PCT/FR90/00762
; FILING DATE: 19-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 8076,84USMO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-9081
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-078-311-1

Query Match 11.6%; Score 139; DB 2; Length 635;

Best Local Similarity 24.0%; Pred.No.9.5e-07;

Matches 59; Conservative 25; Mismatches 76; Indels 86; Gaps 14;

Db 289 LOCFTLIDKNTN-----QMQQ-----DHASSQGFYHSRARCPCPRDRYP 329
QY 61 -----TCHM-----DYHFMAADITFVITIQSGNYSOEGCS-F 93
Db 330 IWENCEEETKNTNPGLOTPQFSRCHFKSRNDSIIHL-----VEYTTAPGVHSTYLSPE 383
QY 94 LLAESIK-PAPPEENVTVTFESGOYNISWRSDYEDPAFYMLKGKIQYELQYRNNG-DPWAVS 151
Db 384 WTHQAVRLPTNLMHREISSGHLEW---QHPSSMAQ-ETCYQLRTYGEHGMKV- 437
QY 152 PRKRLISVDSRSVSLP-----LEFRKDSYELQYRAGPMPGSSYQGTWSEWSDPVI 203
Db 438 -----LEPPLGARGTLELRPRSRVRLQLR-RLNGPTYQGPWSSWSDPTR 482
QY 204 FOTQSE 209
Db 483 VETATE 488

Search completed: June 28, 2002, 07:41:41
Job time: 56 sec

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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:43:19 ; Search time 20.33 Seconds
(without alignments)
415.192 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195
Sequence: 1 CPDLCVCTDYLTQTVICILEM.....SDPVIFQTOSEELKEGNMPH 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	12.1	878	IL3B_MOUSE	P26954 mus musculu
2	144	12.1	896	CYR2_MOUSE	P26955 mus musculu
3	144	12.1	1162	LEPR_MOUSE	P48356 mus musculu
4	141.5	11.8	539	IL2B_MOUSE	P16297 mus musculu
5	139	11.6	635	TPOR_HUMAN	P40238 homo sapien
6	138	11.5	1162	LEPR_HUMAN	O62959 rattus norv
7	137	11.5	1165	LEPR_HUMAN	P48357 homo sapien
8	135.5	11.3	825	IL4R_HUMAN	P24394 homo sapien
9	134	11.2	537	IL2B_RAT	P26956 rattus norv
10	133.5	11.2	369	CYR2_MOUSE	P34902 mus musculu
11	132.5	11.1	625	TPOR_MOUSE	O08351 mus musculu
12	127.5	10.7	379	CYR2_BOVIN	O95118 bos taurus
13	127	10.6	373	CYR2_CANFA	P40321 canis faml
14	126	10.5	551	IL2B_HUMAN	P14784 homo sapien
15	123	10.3	459	IL7R_HUMAN	P16871 homo sapien
16	122	10.2	831	IL6R_MOUSE	O04594 gallus gall
17	122	10.2	918	IL6R_RAT	P40190 rattus norv
18	120	10.0	369	CYR2_HUMAN	P31785 homo sapien
19	118.5	9.9	862	IL2B_HUMAN	O99665 homo sapien
20	118	9.9	897	IL4R_HUMAN	P32927 homo sapien
21	117	9.8	810	IL4R_MOUSE	P16382 mus musculu
22	115.5	9.7	831	IL7R_MOUSE	O91094 melalegris g
23	115	9.6	459	IL7R_MOUSE	P16872 mus musculu
24	112.5	9.4	917	IL6B_MOUSE	O00560 mus musculu
25	110.5	9.2	918	IL6B_HUMAN	P40189 homo sapien
26	108.5	9.1	468	IL6A_HUMAN	P08887 homo sapien
27	106	8.9	638	GHR_PIG	P19756 sus scrofa
28	105.5	8.8	460	IL6A_MOUSE	P22272 rattus norv
29	105.5	8.8	638	GHR_RAT	P16310 rattus norv
30	105	8.8	522	IL9R_HUMAN	O01113 homo sapien
31	104	8.7	638	GHR_RABIT	P19941 coryctolagus
32	103	8.6	508	EPOR_HUMAN	P19335 homo sapien
33	102	8.5	468	IL9R_MOUSE	O01114 mus musculu

34	99.5	8.3	467	IL6A_PIG	O18796 sus scrofa
35	99.5	8.3	507	EPOR_MOUSE	P14753 mus musculu
36	99	8.3	420	IL5R_HUMAN	O01344 homo sapien
37	97.5	8.2	662	IL2R_HUMAN	P42701 homo sapien
38	97	8.1	462	IL6A_RAT	P22273 rattus norv
39	95	7.9	415	IL5R_MOUSE	P21183 mus musculu
40	95	7.9	581	PRUR_CEREL	O28235 cervus elap
41	94	7.9	328	IL2B_MACMU	P46095 macaca mula
42	94	7.9	611	GHR_COLLI	O90375 columba liv
43	93.5	7.8	650	IL5R_MOUSE	P16882 mus musculu
44	93.5	7.8	874	IL2S_MOUSE	P97378 mus musculu
45	93	7.8	327	IL2B_CEREL	O28234 cervus elap

ALIGNMENTS

```

RESULT 1
IL3B_MOUSE STANDARD; PRT; 878 AA.
ID IL3B_MOUSE
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-3 receptor class II beta chain precursor (Colony
DE stimulating factor 2 receptor, beta 2 chain).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90117145; Pubmed=2404337;
RA Itoh N., Yonehara S., Schreurs U., Gorman D.M., Maruyama K., Ishii A.,
RA Yanahara I., Arai K., Miyajima A.:
RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
RT receptor gene family."
RL Science 247:324-327(1990).
CC -1- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
CC RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
CC OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
CC AND GM-CSF RECEPTORS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M29855; AAA39295.1; -
DR PIR: A40091; A40091.
DR MGD: MGI:1339760; Csf2rb2.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR005313; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 878
FT DOMAIN 23 440
FT TRANSMEM 441 462
FT DOMAIN 463 878
FT DISULFID 39 49
FT BY SIMILARITY.

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FT DISULFID 78 95 BY SIMILARITY.
FT DISULFID 254 264 BY SIMILARITY.
FT DISULFID 263 310 BY SIMILARITY.
FT CARBOHYD 350 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 878 AA; 97195 MW; 8EBC9092ADC24D56 CRC64;

Query Match 12.1%; Score 145; DB 1; Length 878;
Best Local Similarity 23.0%; Pred. No. 3.2e-05;
Matches 54; Conservative 30; Mismatches 91; Indels 60; Gaps 9;

QY 4 LVCYDTLVTCILEMMLHPSTLTWQD-----YEE-LKDEATSCSL-- 48
DB 37 LECYNDYTRNIC-----SWADTEDAQGLINMILYHOLDKIOSVCELSE 82
QY 49 -----HRSANHATATYTCNM-----DYHFMAADIFSVNTIDSGNSQSCGSEL 94
DB 83 KLMMSECPSSHRCVPRRCVPTPTRESGNDYYSFOPDDLCIOL-----MVP 130
95 LAESIKPAPFENVTVFSG-QYNISWRSDEDPAYMLKGLQYELQYRNKGDPAVSP 152
131 LAOHVOPPPKDIHISPSGDHFLLEWSVSLGDSVMSLSSKDIIEFEVAYKRLQDSMEDA- 189
QY 153 RRKLISVDSVSLPLLEPKKSSYELQYRAGPMGSSYQGTWSEMDPVIYQOT 207
DB 190 --SLHTSNQVNDPRKFLPNSITARVTRLSAGSSLSGRPSRWSEPVHMSQ 242

RESULT 2
CYRB_MOUSE STANDARD; PRT; 896 AA.
ID CYRB_MOUSE STANDARD; PRT; 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 41, Last annotation update)
DE Cytokine receptor common beta chain precursor.
GN CSF2RB OR CSF2RB1 OR ALC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yabara I., Arai K., Miyajima A.;
RT Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family";
Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: M34397; AAA37204.1; -
DR PIR: A35782; A35782.
DR MGI: MGI:1339759; Csf2rb1.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR003961; FN_III.

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DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 896 CYTOKINE RECEPTOR COMMON BETA CHAIN.
FT DOMAIN 23 441 POTENTIAL.
FT DOMAIN 442 463 POTENTIAL.
FT DOMAIN 464 896 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 132 241 FIBRONECTIN TYPE-III 1.
FT DOMAIN 343 440 FIBRONECTIN TYPE-III 2.
FT DISULFID 39 49 BY SIMILARITY.
FT DISULFID 77 94 BY SIMILARITY.
FT CARBOHYD 62 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 896 AA; 99111 MW; 8CE16DFCC07A999 CRC64;

Query Match 12.1%; Score 144; DB 1; Length 896;
Best Local Similarity 22.6%; Pred. No. 4e-05;
Matches 49; Conservative 41; Mismatches 87; Indels 40; Gaps 9;

QY 3 DLVCYDTLVTCILEMNN-----LHPTLTWQDYEELKDEATSCSLHRS 51
DB 250 NLGCFPDGIDSLGSEWVTQRTGSYFGLFRPAPVA-----PEKSGPVYKEP 299
QY 52 AHNATHTATYTCNMDFVHMADIFSVNTIDSGNSQSCGSLA-SEIKRAPP-FNVTY 109
DB 300 PGASVYTRHCHSLPPEPSAHSGQYTVSVK-----HLGQKFKIMSYNIOMEPTLNLTK 353
QY 110 TFGQYNISWRSDEDPAYMLKGLQYELQYRNKGDPAVSPRRKLISVDSVSLPL 169
DB 354 N-RDSYSLHHEFOKMAVSL-----EHTFQYQYKKKSDSESKTENLDRASMDLS----- 404
QY 170 EPRKDSYELQYRAGPMGSSYQGTWSEMDPVIYQOT 206
DB 405 QLEPDYTSYCARVVKPI--SNYDGIWMSKSEBYTKWT 439

RESULT 3
LEPR_MOUSE STANDARD; PRT; 1162 AA.
ID LEPR_MOUSE STANDARD; PRT; 1162 AA.
AC P48356; O35686; Q61215; Q64309; O54986;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219
DE receptor).
GN LEPR OR OBR OR DB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT A).
RX TISSUE-Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Mair C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Woolf E.A., Montoe C.A., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RT "Identification and expression cloning of a leptin receptor, OB-R";
Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper N.D., Morgenshtern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT identification of a mutation in the leptin receptor gene in db/db

```


RT mice.";
 RL Cell 84:491-495(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (VARIANTS A TO E).
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=96231997; PubMed=8628397;
 RA Lee G.-H., Ploence R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
 RT Lee J.I., Friedman J.M.;
 "Abnormal splicing of the leptin receptor in diabetic mice.";
 RL Nature 379:632-635(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (VARIANT C).
 RC STRAIN=BA1B/C; TISSUE=Liver;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
 RT Mikhail A., Platika D., Snodgrass H.R.;
 "Novel B219/Ob receptor isoforms: possible role of leptin in
 hematopoiesis and reproduction.";
 RT Nat. Med. 2:585-589(1996).
 RP [5]
 RC SEQUENCE FROM N.A. (VARIANT B).
 RX STRAIN=NEW ZEALAND OBESE / NZO; TISSUE=Hypothalamus;
 RT MEDLINE=97462708; PubMed=9322935;
 RA Igel M., Becker W., Herberg L., Joost H.G.;
 RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
 in the New Zealand obese mouse.";
 RL Endocrinology 138:4234-4239(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (VARIANTS A AND B).
 RC STRAIN=FVB/N; TISSUE=Spleen;
 RX MEDLINE=96270520; PubMed=8692797;
 RA Ghilardi N., Ziegler S., Westner A., Stoffel R., Helm M.H.,
 RT Skoda R.C.;
 "Defective STAT signalling by the leptin receptor in diabetic mice.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (VARIANT E).
 RC STRAIN=129/J;
 RX MEDLINE=98008913; PubMed=9344648;
 RA Chua S.C., Koutiras I.K., Han L., Liu S.M., Kay J., Young S.J.,
 RT Chung W.K., Leibel R.L.;
 "Fine structure of the murine leptin receptor gene: splice site
 suppression is required to form two alternatively spliced
 transcripts.";
 RL Genomics 45:264-270(1997).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN
 CC LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.
 CC (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND
 CC LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:
 CC EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U42467; AAA93014.1; -
 CC EMBL; U46135; AAC52408.1; -
 CC EMBL; U49106; AAC52420.1; -
 CC EMBL; U49107; AAC52421.1; -

DR EMBL; U49108; AAC52422.1; -
 DR EMBL; U49109; AAC52423.1; -
 DR EMBL; U49110; AAC52424.1; -
 DR EMBL; U52915; AAC52599.1; -
 DR EMBL; Y10298; CAA71343.1; -
 DR EMBL; U58861; AAC52705.1; -
 DR EMBL; U58862; AAC52706.1; -
 DR EMBL; U58863; AAC52707.1; -
 DR EMBL; AF039456; AAB95334.1; -
 DR EMBL; AF039443; AAB95334.1; JOINED.
 DR EMBL; AF039444; AAB95334.1; JOINED.
 DR EMBL; AF039445; AAB95334.1; JOINED.
 DR EMBL; AF039446; AAB95334.1; JOINED.
 DR EMBL; AF039447; AAB95334.1; JOINED.
 DR EMBL; AF039448; AAB95334.1; JOINED.
 DR EMBL; AF039449; AAB95334.1; JOINED.
 DR EMBL; AF039450; AAB95334.1; JOINED.
 DR EMBL; AF039451; AAB95334.1; JOINED.
 DR EMBL; AF039452; AAB95334.1; JOINED.
 DR EMBL; AF039453; AAB95334.1; JOINED.
 DR EMBL; AF039454; AAB95334.1; JOINED.
 DR EMBL; AF039455; AAB95334.1; JOINED.
 DR HSSP; P40189; IBOU.
 DR MCD; MG1:104993; Lepr.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam; Pf00041; fn3; 3.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 DR Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Polymorphism; Alternative splicing.
 KW SIGNAL 1 21
 FT CHAIN 22 1162
 FT DOMAIN 22 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821
 FT CARBOHYD 41
 FT CARBOHYD 56
 FT CARBOHYD 73
 FT CARBOHYD 98
 FT CARBOHYD 187
 FT CARBOHYD 275
 FT CARBOHYD 345
 FT CARBOHYD 431
 FT CARBOHYD 514
 FT CARBOHYD 622
 FT CARBOHYD 657
 FT CARBOHYD 668
 FT CARBOHYD 686
 FT CARBOHYD 695
 FT CARBOHYD 698
 FT CARBOHYD 726
 FT CARBOHYD 890
 FT CARBOHYD 895
 FT CARBOHYD 890
 FT CARBOHYD 892
 FT CARBOHYD 893
 FT CARBOHYD 900
 FT VARSPLIC 901 1162
 FT VARSPLIC 797 805
 FT VARSPLIC 806 1162
 FT VARIANT 541 541
 FT VARIANT 651 651
 FT VARIANT 1044 1044
 FT VARIANT 140 140
 FT CONFLICT 720 720
 FT SEQUENCE 1162 AA; 130788 MW; 0E1E75B076BA60A2 CRC64;
 D).
 MISSING (IN THE ISOFORM D).
 DNEPIRYK -> GMCVLPMD (IN ISOFORM E).
 MISSING (IN ISOFORM E).
 V -> I (IN STRAIN NO2).
 V -> I (IN STRAIN NO2).
 T -> I (IN STRAIN NO2).
 F -> I (IN REF. 6).
 A -> P (IN REF. 5).
 MISSING (IN ISOFORM C).
 PETEFLFTN -> DISHEVFLFR (IN ISOFORM
 D).

Query Match 12.1%; Score 144; DB 1; Length 1162;
 Best Local Similarity 31.1%; Pred. No. 5,6e-05;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

39 LKBE-----ATSCSLHRSANNAHTATYCHMDVPH-----EMADIFSVNITDGSNGNS 87
 177 LKSFQVQVNCNCLRGC-----ECHVPPRAKLNALMLYETISAGVSFQSPPLMS 227
 88 QECGSELLAEIRKAPP--FNVTYFSGQYNISWRSDYEDPAFYMLKCKLQYELQYRNG 145
 228 LQ--PMLV---VKDPDPLGLHMEVTDGMLKISMDSQTWAPP-----PLYQVYKLENS 276
 146 DPAVSEPRKLVSDRSV-SLLPLEFRKDSYELQVRAGPMPGSSYQCTSEMSDPYIF 204
 277 T--TVREAAIVATSLVDVSLP-----GSSTEVQVNRKRLDGS---GWSWSSDPQVF 326

QY 205 QVQ 207
 DB 327 TTQ 329

RESULT 4
 ID IL2B_MOUSE STANDARD; PRT; 539 AA.
 AC P16297;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122).
 GN IL2RB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90175385; PubMed=2155425;
 RA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,
 RA Miyazaki M., Miyata T., Taniguchi T.;
 RT "Murine interleukin 2 receptor beta chain: dysregulated gene
 expression in lymphoma line EL-4 caused by a promoter insertion.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
 INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
 MITOGENIC SIGNALS OF IL-2.
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 WITH A GAMMA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 or send an email to license@sib-sib.ch).
 CC EMBL: M28052; AAA39283.1; -
 DR PTR: A35052; A35052.
 DR HSSP: P14784; 11LN.
 DR MGD: MGI:96530; 11ZD.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 26
 FT CHAIN 27 539
 FT DOMAIN 27 240
 FT TRANSSEM 241 268
 FT DOMAIN 269 539
 FT DISULFID 36 46
 FT DISULFID 74 86
 FT CARBOHYD 30 30
 FT CARBOHYD 43 43
 FT CARBOHYD 55 55
 FT CARBOHYD 71 71
 FT CARBOHYD 150 150
 FT CARBOHYD 216 216
 SO SEQUENCE 539 AA; 60538 MM; 365C9D20686BE14 CR664;

Query Match 11.8%; Score 141.5; DB 1; Length 539;
 Best Local Similarity 22.5%; Pred. No. 3,6e-05;
 Matches 54; Conservative 43; Mismatches 86; Indels 57; Gaps 12;

QY 1 CPDLYCTDYLYQVYCIEMNNLHPSTLITWQDYELKDEATSCSLHRSANNAHTATY 60
 DB 31 CSHLECFYNSRANVSC---WMS-HEEALNV-----TTCVHAKS-NLRHMK 72
 QY 61 TCHMDVPH-----FMADIFSVNIT--DQSGNYSOCGSEFLAESIK 100
 DB 73 TCETLIVROASMACNLIIGSPESQSLTSDLDINVCMEEGMRVKTCDHFPPDNR 132
 QY 101 PAPPFNTVTF--SGQYNISWR---SDYEDPAFYMLKCKLQYELQYRNGPMAVSPR 154
 DB 133 LVAPHSLQVLAHIDTQRNCNISMKVSQVSHYTEP-----YLEEFARRLIGSHWDA-- 182
 QY 155 KLIVDSRSVSLPLEFRKDSYELQVRAGPMPGSSYQCTSEMSDPYIFQV-SEELKE 213
 DB 183 SVSLKQRQWLFLEMLIPSTSYEVQVRVKAQRNNI--GTWSWSPQLPFRFRPADPKME 240

RESULT 5
 ID TPOR_HUMAN STANDARD; PRT; 635 AA.
 AC P40238;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
 protein) (C-mpl) (CD110 antigen).
 GN MPL OR TPOR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92302297; PubMed=1608974;
 RA Vigon I., Morron J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
 RA Gisselbrecht S., Souyri M.;
 RT "Molecular cloning and characterization of MPL, the human homolog of
 the v-mpl oncogene: identification of a member of the hematopoietic
 growth factor receptor superfamily.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
 CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
 MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C-MPL-K (SHOWN HERE) AND C-MPL-
 P. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF

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Query March 11.6% Score 139; DB 1; Length 635;
Best Local Similarity 24.0% Pred No 7.3e-05;
Matches 59; Conservative 25; Mismatches 76; Indels 86; Gaps 14

QY      4  IVCYTDYQIVYICILEMMNHPSTLTITWODQYELKDEATSCSL--HRSANHTATY- 60
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      289  LQCFEFLDKNVTCT-----QWQOQ-----DHASQGFHYHSRARCPRDRYP 329
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY      61  -----TCHM-----DYFHEMADDSFVNITDQSGNYSQECS-F 93
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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Db 330 IMNCCEEEKTIPGQIQTQFQRCHFKSRNDSIIHLL-----VEVYTAAGVHSTIGSPF 383
Oy 94 LLAESIK-PAPEPNTVYFSGOYNIMSRSDYEDPAFYMKGKLOLEYLRNRNG-DPMAYVS 151
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 384 WIIQANRLPTPLMLHRELSSCHLELW-----QHPSSMAN-ETCYQALRTGEGHQDMKV- 437
Oy 152 PRKKLISVDNSVSLP-----LEPRKDSYEIVQNRAGPFGSSIQGTWSEKSDPYI 203
Db 438 -----LEPLGARGGTLELRPSRRYRLQRA-RLNGPTVQGPWSSWSDPFR 482
Oy 204 FOTQSE 209
Y : : :
Db 483 VERATE 488

RESULT 6
LEPR_RAT STANDARD: PRT: 1162 AA.
ID LEPR_RAT AC Q62959; Q63007; P70493; P70494; P70495; Q63385; Q63386; Q54805;
AC P97589; Q35772;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DT Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEPR OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Hypothalamus;
RX MEDLINE=96241565; PubMed=8673096;
RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
RA Hess J.P.,
RT "Leptin receptor missense mutation in the fatty Zucker rat.";
RL Nat. Genet. 13:18-19(1996).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN=SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE=Brain;
RX MEDLINE=96295531; PubMed=8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Substitution at codon 269 (glutamine -> proline) of the leptin
RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
RT (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
RC STRAIN=SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE=96332408; PubMed=8769097;
RA Takaya K., Ogawa Y., Issse N., Okazaki T., Satoh N., Masuzaki H.,
RA Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary
RT DNAs - identification of a missense mutation in Zucker fatty (fa/fa)
RT rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT B).
RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
RA Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
RC STRAIN=SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE=96212906; PubMed=8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
RT Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
RN [6]
RP SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;

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RT "Analysis of rat leptin receptor gene."
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 694-878 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
 RA Ma Z.;
 RT "Identification of a leptin receptor in islet."
 RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Chien E.K., Hara M., Rouard M., Yano H., Philippe M., Polonsky K.S.,
 RL Bell G.I.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RN [9]
 RP VARIANT PA PRO-269
 RX MEDLINE-96314329; PubMed-8690163;
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.;
 "Phenotype of fatty due to Glu269Pro mutation in the leptin receptor
 (Lepr).";
 CC Diabetes 45:1141-1143(1996).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
 CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHYTERING
 CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
 CC TISSUE.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: U52966; AAC52587.1; -
 DR EMBL: D84350; BAA12637.1; -
 DR EMBL: D84551; BAA12698.1; -
 DR EMBL: D85557; BAA12830.1; -
 DR EMBL: D85558; BAA12831.1; -
 DR EMBL: D85559; BAA12832.1; -
 DR EMBL: U60151; AAB06616.1; -
 DR EMBL: D84125; BAA12230.1; -
 DR EMBL: D84126; BAA12231.1; -
 DR EMBL: AB011006; BAA24899.1; -
 DR EMBL: U67207; AAB40654.1; -
 DR EMBL: AF007818; AAB63201.1; -
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 2.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 DR Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KM Polymorphism; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 1162
 FT DOMAIN 22 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821

FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 695 695 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 890 894 MISSING (IN ISOFORM A).
 FT VARSPLIC 895 892 PET -> VTV (IN ISOFORM A).
 FT VARSPLIC 893 1162 MISSING (IN ISOFORM C).
 FT VARSPLIC 797 805 DNFTPIERY -> GMCVTLIN (IN ISOFORM E).
 FT VARSPLIC 806 1162 MISSING (IN ISOFORM E).
 FT VARIANT 269 269 Q -> P (IN FA).
 FT CONFLICT 2 2 T -> M (IN REF. 4).
 FT CONFLICT 12 12 H -> P (IN REF. 6).
 FT CONFLICT 34 34 K -> R (IN REF. 6).
 FT CONFLICT 751 732 CV -> SL (IN REF. 7).
 FT CONFLICT 846 846 I -> V (IN REF. 8).
 FT SEQUENCE 1162 AA; 130832 MM; BA7AC20A2D2E2A2F CRC64;
 Query Match 11.5%; Score 138; DB 1; Length 1162;
 Best Local Similarity 30.9%; Pred. No. 0.0019;
 Matches 56; Conservative 23; Mismatches 62; Indels 40; Gaps 11;
 QY 39 LKD--EATSCSLHRSANHTATYTCCHMDYR-----FPAADIFSVNTTDDSGNYSOE 89
 DB 177 LKSFQVQO-----NCSVRECEHVPVPRAKYNVALMYLETITSAVGSFSPMSIQ 229
 QY 90 CGSFLAESIKPAP--FNVTVTFSCQYNISWSPDEDPAFYMLKGLQYELQYRRNGDP 147
 DB 230 --PLTV---VKPPPLGLRMEVETDGNLKLISWDSQTKAP-----PLYQVYRLNST- 277
 QY 148 WAYSFRKLIVDSRSV-SLPLERKDSYELQVRAQPMGSSYQSTWMSDPVIFQT 206
 DB 278 -IYREAEIVSDTSLVDSVLP-----GSSIEVQYRKRLDGS--GWSDMSLPOLFTT 328
 QY 207 Q 207
 DB 329 Q 329
 RESULT 7
 LEPR_HUMAN STANDARD; PRT; 1165 AA.
 ID LEPR_HUMAN
 AC P48357;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
 GN LEPR OR OBR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-96128129; PubMed-8548812;
 RA Tartaglia L.A., Dembeki M., Meng X., Deng N., Culpepper J.,
 RA Deyos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
 RA Mufi C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,

DR	EMBL:	U59252;	AAB09673.1.	JOINED.
DR	EMBL:	U59253;	AAB09673.1.	JOINED.
DR	EMBL:	U59254;	AAB09673.1.	JOINED.
DR	EMBL:	U59255;	AAB09673.1.	JOINED.
DR	EMBL:	U59256;	AAB09673.1.	JOINED.
DR	EMBL:	U59257;	AAB09673.1.	JOINED.
DR	EMBL:	U59258;	AAB09673.1.	JOINED.
DR	EMBL:	U59259;	AAB09673.1.	JOINED.
DR	EMBL:	U59260;	AAB09673.1.	JOINED.
DR	EMBL:	U59261;	AAB09673.1.	JOINED.
DR	HSSP:	P40189;	1BQV.	
DR	MIM:	601007;	-	
DR	InterPro:	IPR002996;	CRIA.	
DR	InterPro:	IPR003961;	FN.III.	
DR	InterPro:	IPR003529;	Hematopo_receptor_L_F2.	
DR	Pfam:	PF00041;	fns_2.	
DR	SMART:	SM00060;	PN3_1.	
DR	PROSITE:	PS01353;	HEMATOPO_REC_L_F2; 1.	
KM	Oestry:	Receptor;	Transmembrane; Glycoprotein; Signal; Repeat;	
FT	Polyomorphism.	1	21	
FT	SIGNAL	22	1165	POTENTIAL.
FT	CHAIN	22	841	LEPTIN RECEPTOR.
FT	DOMAIN	22	841	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	842	862	POTENTIAL.
FT	DOMAIN	863	1165	CYTOSOLASMIC (POTENTIAL).
FT	DOMAIN	237	320	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	537	623	FIBRONECTIN TYPE-II 2.
FT	DOMAIN	738	823	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	23	23	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	56	56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	73	73	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	81	81	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	247	247	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	433	433	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	516	516	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	659	659	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	688	688	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	697	697	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	728	728	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	109	109	K -> R.
FT	VARIANT	204	204	/FTID=VAR..002703.
FT	VARIANT	223	223	K -> R.
FT	VARIANT	656	656	/FTID=VAR..002704.
FT	VARIANT	675	675	Q -> R.
FT	VARIANT	675	675	/FTID=VAR..002705.
FT	VARIANT	675	675	K -> N.
FT	VARIANT	675	675	/FTID=VAR..002706.
FT	VARIANT	675	675	S -> T.
FT	VARIANT	675	675	/FTID=VAR..002707.
SO	SEQUENCE	1165 AA;	132449 MW;	8FF21D9AF512S808 CRC64;
QY	Query Match	11.58;	Score 137;	DR 1; Length 1165;
DB	Best Local Similarity	28.08;	Pred. No. 0.00023;	
Matches	47; Conservative	25;	Mismatches 68;	Indels 28; Gaps
QY	45	SCSLHSANNAHATATTC	HMDFEFIFNADD-	IFSUNITDSGNSOECSFLLAESTIKPA 102
DB	187	NCSEVHCCE-----	CLVEVPKANTPLTLMCKI	TSGGVIFOSFLMSVOPIMWVRPD 238
QY	103	PP--FNTTYFGGOYNISMRSDY	DDPAFWLKGKLOYTELOYRNNGDPMAVS	PRKLUSVD 160
DB	239	PLGLIMEHTTDGDNKIKISMSP-----	RIVPEPPLQYOYKI-SNLSITYIR	REMDIVAVAT 291

Oy 161 SRSV-SLLPFRKDSYELAVRAGPMGSSSYOGTWSNSDPYIPOTQ 207
 Db 292 SLVSDILP-----GSSIEYQYKGRKLDG---FQINSMDSTPRTFTQ 331
 RESULT 8
 IL4R_HUMAN STANDARD: PRT; 825 AA.
 AC P24394;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen)
 GN IL4R OR IL4RA OR 582J2.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE=Peripheral blood;
 MEDLINE=90171849; PubMed=2307934;
 RA Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V., Gimpel S.D., Din W.S., Grabstein K.H., Wilder M.B., Park L.S., Cosman D., Beckmann M.P.;
 RA "Human interleukin 4 receptor confers biological responsiveness and defines a novel receptor superfamily.";
 RT J. Exp. Med. 171:861-873(1990).
 RN [2]
 SEQUENCE FROM N.A.
 MEDLINE=91120547; PubMed=2278997;
 RA Galizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O., Kastelein R., Banchereau J., Howard M., Miyajima A.;
 RA "Molecular cloning of a cDNA encoding the human interleukin 4 receptor.";
 RT Int. Immunol. 2:669-675(1990).
 RN [3]
 SEQUENCE FROM N.A.
 MEDLINE=99425270; PubMed=9070874;
 RA Loftus B.J., Kim U.-T., Sneedon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Crohn L., Deslattes Mays R., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Elcher E.E., Harris P.C., Venter J.C., Adams M.D.;
 RA "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
 RT Genomics 60:295-308(1999).
 RN [4]
 VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
 MEDLINE=97224413; PubMed=9070874;
 RA Deichmann K., Bardutzky J., Forster J., Heinemann A., Kuehr J.;
 RA "Common polymorphisms in the coding part of the IL4-receptor gene.";
 RT Biochem. Biophys. Res. Commun. 231:696-697(1997).
 RN [5]
 VARIANT ATOPIC ARG-576.
 MEDLINE=98041803; PubMed=9392697;
 RA Hershley G.K.K., Friedrich M.F., Esswein L.A., Thomas M.L., Charlita T.A.;
 RA "The association of atopy with a gain-of-function mutation in the alpha subunit of the interleukin-4 receptor.";
 RT New Engl. J. Med. 337:1720-1725(1997).
 RN [6]
 VARIANT ATOPIC ASTHMA VAL-75.
 MEDLINE=98282087; PubMed=9620765;
 RA Matsuyasu H., Izuhara K., Mao X.-O., Gao P.S., Arihara Y., Enomoto T., Kawai M., Sasaki S., Dake Y., Hamaoka N., Shirakawa T., Hopkin J.M.;
 RA "H505Val variant of IL4R alpha upregulates Ige synthesis and associates with atopic asthma.";
 RT Nat. Genet. 19:119-120(1998).
 RN [7]
 VARIANT ATOPIC ASTHMA VAL-75.
 MEDLINE=99322293; PubMed=10390422;
 RA Noguchi E., Shibasaki M., Ariuami T., Takeda K., Yokouchi Y., Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.;
 RA "No association between atopy/asthma and the H505Val polymorphism of IL-4 receptor.";
 RT Am. J. Respir. Crit. Care Med. 160:342-345(1999).
 RN [8]
 VARIANTS PRO-503 AND ARG-576.
 MEDLINE=99250314; PubMed=10233717;
 RA Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J., Deichmann K.A.;
 RA "The polymorphisms S503P and Q576R in the interleukin-4 receptor alpha gene are associated with atopy and influence the signal transduction.";
 RT Immunology 96:365-371(1999).
 RN [9]
 VARIANT ALA-752.
 MEDLINE=20143377; PubMed=10677312;
 RA Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Daniel R., Newman D.L., Wu X., Parry R., Lester U.A., Solway J., Blumenthal M., King R.A., Xu J., Meyers D.A., Blecker E.R., Cox N.J.;
 RA "Variation in the interleukin 4-receptor alpha gene confers susceptibility to asthma and atopy in ethnically diverse populations.";
 RT Am. J. Hum. Genet. 66:517-526(2000).
 RN [10]
 VARIANT ATOPIC ARG-576.
 MEDLINE=20269830; PubMed=10809862;
 RA Oiso N., Fukai K., Ishii M.;
 RA "Interleukin 4 receptor alpha chain polymorphism Gln551Arg is associated with adult atopic dermatitis in Japan.";
 RT Br. J. Dermatol. 142:1003-1006(2000).
 RN [11]
 VARIANT PRO-786.
 MEDLINE=21405389; PubMed=11513543;
 RA Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M., Brzezinski J.L., Bernstein J.A., Khurana Hershley G.K.;
 RA "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic variant in allergic and nonallergic asthma and its functional consequences.";
 RT Clin. Immunol. 100:298-304(2001).
 RN [12]
 VARIANT ILE-579.
 MEDLINE=21182061; PubMed=11285129;
 RA Lozano F., Peces de la Iglesia A., Misericachs N., Vives J., Suarez B., Lopez de la Iglesia A., Misericachs N., Vives J.;
 RA "Identification of a novel single-nucleotide polymorphism (Val554Ile) and definition of eight common alleles for human IL4RA exon 11.";
 RT Tissue Antigens 57:216-220(2001).
 RN [13]
 FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-4. A SOLUBLE FORM OF THE IL-4 RECEPTOR MAY REPRESENT A REGULATORY MOLECULE SPECIFIC FOR IL-4-DEPENDENT IMMUNE RESPONSES.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: DEFECTS IN IL4R ARE A CAUSE OF ATOPIC ASTHMA.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROT; NOTE-CD guide CD124 entry; WWW="http://www.ncbi.nlm.nih.gov/prot/cd/cd124.htm"
 CC
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 CC
 CC EMBL: X52425; CAA36672.1; -
 CC EMBL: AC004525; AAC23495.1; -
 DR PIR: A60386; A60386.
 DR PIR: A47603; A47603.
 DR MIM: 147781; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.

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DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
KW Polymorphism.
FT SIGNAL 1 25
FT CHAIN 26 825
FT DOMAIN 26 232
FT TRANSMEM 233 256
FT DOMAIN 257 825
FT DISULFID 34 44
FT DISULFID 74 86
FT CARBOHYD 53 53
FT CARBOHYD 98 98
FT CARBOHYD 128 128
FT CARBOHYD 134 134
FT CARBOHYD 176 176
FT CARBOHYD 209 209
FT CARBOHYD 75 75
FT VARIANT 400 400
FT VARIANT 431 431
FT VARIANT 436 436
FT VARIANT 503 503
FT VARIANT 576 576
FT VARIANT 579 579
FT VARIANT 752 752
FT VARIANT 786 786
FT VARIANT 786 786
SQ SEQUENCE 825 AA; 89658 MM; 9F86DF5612297F8 CRC64;

Query Match 11.3%; Score 135.5; DB 1; Length 825;
Best Local Similarity 26.0%; Pred. No. 0.00021;
Matches 57; Conservative 25; Mismatches 76; Indels 61; Gaps 12;

OY 6 CTTTQVLTQVLTICILEMNNLHPST-----LTLTQDQYELKDEATSCSLHRSANNTATY 60
OY 34 CVDYSNLSISYC--EMKMGPTNGSTELRLYLQVLF--LSEAHATC-----IRENNGAGC 84
OY 61 TCHHDDVHFMAADDIFSNNITDQSGNTSOEC-----GSLFLASIKRPAPFVNTY-- 109
OY 85 VCHL-----LMDVVSAD-----NYTLDMAGQQLLTKSGSFKEHVPRAPGMLTVHT 133
OY 110 TFSQGVNISMRSDEYDPAFYWLKKGLOYELQYRNGDPMWASPRKLISVDSRSVLLPL 169
OY 134 NVSTQTLTMSNPY--PPDNYLVNHLTVANIMSENDE-----ADPRINVTYVL 180
OY 170 E-----FRKDSYELQYRAGPAGSSYOGTSEMS 199
OY 181 EPSLRIZASTLKSIGISYRARVAM--AQCYNVTSEMS 216

RESULT 9
IL2B_RAT STANDARD: PRT; 537 AA.
AC P26896;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
DE (High affinity IL-2 receptor beta subunit) (CD122).
GN IL2RB.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RX MEDLINE-91364784; PubMed-1869461;
RA Page T.H., Dallman M.J.;
RT "Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha
RT and beta chain genes: differentially regulated gene activity in
RT response to mitogenic stimulation."
RL Eur. J. Immunol. 21:2133-2138(1991).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
CC INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
CC MITOGENIC SIGNALS OF IL-2.
CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb.sdb.ch).
CC -----
DR EMBL: M55050; AAA41429.1; -
DR HSPB: P14784; IITN
DR InterPro: IPR002996; CR1A
DR InterPro: IPR003951; FN.III
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 537
FT DOMAIN 27 239
FT TRANSMEM 240 267
FT DOMAIN 268 537
FT DISULFID 36 46
FT DISULFID 74 86
FT CARBOHYD 43 43
FT CARBOHYD 55 55
FT CARBOHYD 71 71
FT CARBOHYD 150 150
SQ SEQUENCE 537 AA; 60657 MM; 9C744A24F3361968 CRC64;

Query Match 11.2%; Score 134; DB 1; Length 537;
Best Local Similarity 23.1%; Pred. No. 0.00016;
Matches 58; Conservative 41; Mismatches 72; Indels 80; Gaps 13;

OY 1 CPDLVCTVLTQVLTICILEMNNLHPSTLTLTQDQYELKDEA---TSCSLHRSAN----- 53
OY 31 CSHLKEFYNSRANVSC--WMS-----PEBALNTSCHIHAQSDMRHW 70
OY 54 NAT-----HATYTCNM-----DVFHFMAADDIFSNNIT--DQSGNTSOECGSLAAS 98
OY 71 NKTCELTPYKQASMACNLLGLPDPQSLSVLDLSTLSYCWKEKMRVYKTCFFHFDN 130
OY 99 IKRPAPFVNTYTF--SGOYNLSWR-----SDYEDPAFYWLKKGLOYELQYRNGDPMWAVSP 152
OY 131 LNLAPHSIGVLIHTIRCNISMVYSQVSHYNP-----YLEFF-----A 170
OY 153 RRLKISVDSRSVLLPLEFR-----DSYELQYRAGPAGSSYOGTSEMSGDPV 202
OY 171 RRLILDRSWEASVSLKQKQOMFLPELTLPDTSTELQVRYIAQKSKT--RTWSPMSQPM 228
DB 171 RRLILDRSWEASVSLKQKQOMFLPELTLPDTSTELQVRYIAQKSKT--RTWSPMSQPM 228

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QY	203	INFOSEQUENCE 213
Db	229	APRTRPADPKE 239
RESULT 10		
AC	CYRG-MOUSE	STANDARD: PRG: 369 AA.
DT	01-FEB-1994 (Rel. 28, Created)	
DT	01-FEB-1994 (Rel. 28, Last sequence update)	
DT	15-DEC-1998 (Rel. 37, Last annotation update)	
DE	Cytokine receptor common gamma chain precursor (Gamma-C)	
DE	(Interleukin 2 receptor gamma chain) (IL-2R gamma chain) (p64).	
GN	IL2RG.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID:10090.	
RN	(1)	
RN	SEQUENCE FROM N.A.	
RN	MEDLINE-93377575; PubMed-8503926;	
RN	Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;	
RN	"Cloning of the mouse interleukin 2 receptor gamma chain:	
RN	demonstration of functional differences between the mouse and human	
RN	receptors.";	
RN	Biochem. Biophys. Res. Commun. 193:356-363(1993).	
RN	(2)	
RN	SEQUENCE FROM N.A.	
RN	SPRAIN-CBA/CA.	
RN	MEDLINE-93393174; PubMed-8378320;	
RN	Cao X., Kosak C.A., Liu Y.T., Noguchi M., O'Connell E., Leonard W.T.;	
RN	"Characterization of cDNAs encoding the murine interleukin 2 receptor	
RN	(IL-2R) gamma chain: chromosomal mapping and tissue specificity of	
RN	IL-2R gamma chain expression.";	
RN	Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).	
RN	(3)	
RN	SEQUENCE FROM N.A.	
RN	MEDLINE-93366191; PubMed-8359699;	
RN	Kobayashi N., Nakagawa S., Mimami Y., Taniguchi T., Kono T.;	
RN	"Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor	
RN	gamma.";	
RN	gene 130:303-304(1993).	
RN	(4)	
RN	SEQUENCE FROM N.A.	
RN	MEDLINE-95104285; PubMed-7805729;	
RN	Disanto J.P., Certain S., Wilson A., MacDonald H.R., Avner P.,	
RN	Rischer A., de Saint Basile G.;	
RN	"The murine interleukin-2 receptor gamma chain gene: organization,	
RN	chromosomal localization and expression in the adult thymus.";	
RN	Eur. J. Immunol. 24:3014-3018(1994).	
RN	(5)	
RN	SEQUENCE FROM N.A.	
RN	SPRAIN-B6.S;	
RN	MEDLINE-96341745; PubMed-8750189;	
RN	Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,	
RN	Dougherty G.J.;	
RN	"Molecular mechanisms regulating the hyaluronan binding activity of	
RN	the adhesion protein CD44.";	
RN	J. Neuroconol. 26:231-239(1995).	
RL	J. FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF	
CC	INTERLEUKINS.	
CC	-1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND	
CC	PROBABLY ALSO THE IL-13 RECEPTORS.	
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
CC	-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.	
CC	-----	
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CC	modified and this statement is not removed. Usage by and for commercial	

[illegible]

DE protein) (C-mpl).
 GN MPL OR TPOR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93327753; PubMed=8334987;
 RA Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
 RA Leder P.;
 RT "Murine c-mpl: a member of the hematopoietic growth factor receptor
 RT superfamily that transduces a proliferative signal.";
 RL EMBO J. 12:2645-2653(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ICFW; TISSUE=Petal liver;
 MEDLINE=93390934; PubMed=8397366;
 RA Vigon I., Florindo C., Fichelson S., Guenet J.-L., Mattle M.-G.,
 RA Souyri M., Cosman D., Gisselbrecht S.;
 RT "Characterization of the murine Mpl proto-oncogene, a member of the
 RT hematopoietic cytokine receptor family: molecular cloning,
 RT chromosomal location and evidence for a function in cell growth.";
 RL Oncogene 8:2607-2615(1993).
 CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
 CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 DR EMBL: 222649; GAA80365.1; -;
 DR EMBL: 222657; GAA80372.1; -;
 DR EMBL: 273677; GAA52031.1; -;
 DR PIR: S35317; S35317.
 DR HSSP: P19235; 1EBA.
 DR MGD: MGI:97076; Mpl.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003528; Hematopo_receptor_L.F1.
 DR Pfam: PF00041; fn3.1.
 DR SMART: SM00060; FN3.1.
 DR PROSITE: PS01352; Hematopo_REC_L.F1.1.
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 25
 FT CHAIN 1 25
 FT DOMAIN 26 625
 FT TRANSMEM 26 482
 FT DOMAIN 483 504
 FT DOMAIN 505 625
 FT CARBOHYD 117 117
 FT CARBOHYD 2 8
 FT CONFLICT 99 99
 FT CONFLICT 222 222
 FT CONFLICT 222 222
 FT SEQUENCE 625 AA; 69817 MW; 309CFE6EA3724549 CRC64;
 SO
 Query Match 11.18; Score 132.5; DB 1; Length 625;
 Best Local Similarity 25.08; Pred. No. 0.00027;
 Matches 60; Conservative 25; Mismatches 80; Indels 75; Gaps 14;
 OY 4 LVCYDYLYQVYICILEMMNHPSTLTJTWODQELKDEATSLRSANMTHATY-- 61
 DB 281 LQCFLLDKAMKTC-----QWQOO-----DRSSGSGFR--HSNRRCPTDR 319
 OY 62 -----CHM-----DVFFHMAADIFSVNITDQSGNSQSCGS- 92

DB 320 DEPWKECEEEPRRCSOPALYSRCHFRKSRNDSVHIL-----VEVTTAQAGVHSYLSP 373
 OY 93 FLIAEST-KPAPFNVVTFESGQYNISMSRSDYEDPAPYMKGLQYELQRYNRG-DPMAY 150
 DB 374 FWHQAVLLPPTSLHMRREVSSGRLEFMOHQSSWA-----QETCYQLRYTEBGRDKV 428
 OY 151 -SPRRKLISVDSRSYSLILPEFRKDSSEYLOVRAGPMPGSSYGGTSEMSDPVIFQTOSE 209
 DB 429 LEP-----SLARGST---LELRPRARYSLQLR-RUNGFTYGGPMSANSPARVSTGSE 479
 RESULT 12
 ID CYRG_BOVIN STANDARD; PRT; 379 AA.
 AC 095118;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (p64).
 GN IL2RG.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96268473; PubMed=8672241;
 RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
 RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
 RT gamma gene.";
 RL DNA Cell Biol. 15:453-459(1996).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U33748; AAB07812.1; -;
 DR HSSP: P31785; 1ILN.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003531; Hematopo_receptor_S.F1.
 DR Pfam: PF00041; fn3.1.
 DR SMART: SM00060; FN3.1.
 DR PROSITE: PS01355; Hematopo_REC_S.F1.1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 1 379
 FT DOMAIN 23 269
 FT TRANSMEM 270 290
 FT DOMAIN 291 379
 FT DOMAIN 158 256
 FT DISULFID 68 78
 FT DISULFID 109 122
 FT CARBOHYD 77 77
 FT CARBOHYD 81 81
 FT CARBOHYD 90 90
 FT CARBOHYD 156 166
 FT CARBOHYD 171 171
 FT SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;
 SO

RA Grafham D., Griffiths M.N., Hall C., Hall R., Hall-Tamlyn G.,
RA Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Leverish M.A.,
RA Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M.,
RA Matthews L., Mccann O.T., Mcclellan J., McLaren S., Mccormick A.A.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsey H.,
RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Sulston J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M.,
RA Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
RA Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E.,
RA Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D.,
RA Wu H., Yao Z., Zhan M., Zhang G., Chisoe S., Murray J., Miller N.,
RA Minx P., Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H.,
RA Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
RA Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P.,
RA Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K.,
RA Nelson J., Korf I., Bedell J.A., Hilder L., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saita S.,
RA Budarf M.L., Mederid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dunamski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Brider C.E.,
RA O'Brien K.P., Wilkinson P., Bodenleitch A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [3]
RP 3D-STRUCTURE MODELING OF 31-230.
RX MEDLINE=95111955; PubMed=7529123;
RA Bamorough P., Hedgecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
RT modelling.";
RL Structure 2:839-851(1994).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
CC INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
CC MITOGENIC SIGNALS OF IL-2.
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD122 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd122.htm".
CC -----
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CC -----
CC EMBL: M26062; AAA59143.1; -;
DR EMBL: A1022314; CAAL8444.1; -;
DR PIR: A30342; A30342.
DR PDB: 1ILN; 26-JAN-95.
DR MIM: 146710; -;
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.

FT SIGNAL 1 26
FT CHAIN 27 551 INTERLEUKIN-2 RECEPTOR BETA CHAIN.
FT DOMAIN 27 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 265 POTENTIAL.
FT DOMAIN 266 551 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 68 312 PRO/SER-RICH.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 74 86 BY SIMILARITY.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 551 AA; 61117 MW; 1A76FA1936BB7EE6 CRC64;

Query Match 10.5%; Score 126; DB 1; Length 551;
Best Local Similarity 23.6%; Pred. No. 0.00087;
Matches 51; Conservative 39; Mismatches 92; Indels 34; Gaps 11;

QY 26 SNTLTWQDQVEELKDEAFSCSIH---RSAHNT-----HATYTCM-----DYFHF 69
DB 42 ANISCVW-SQCGALQD--TSCVHAMPRRRNQCETLPYQSASMACNLILGAPDSQKL 98
QY 70 MADDFSVNITDQSGNYSQEGC--SELLAESIKPAPPNVTYTF--SQQYNIWSRSDYED 125
DB 99 TTVDTIVTLRVLCREGVRRVMAIQDFKPFENLRMAPISLQVHVETHRCNISWEI--S 155
QY 126 PAFYMLKGLQYELQYRRNGPWNVSPRRKLISYDSRSVSLPLEFRDSSYELOVRAP 185
DB 156 QASHFEERLEFEATLTSPGHTEAP--LITLKQKEWICLETLPDITYEFOVRVKKP 212
QY 186 MPGSSYOGTSEMSDPVIFOFQSEELKEG---WNPH 218
DB 213 LQGER--TTWSPWSQPLAFRTKPAALGKDTIPWLG 246

RESULT 15
ID IL2R_HUMAN STANDARD: PRT; 459 AA.
AC P16871;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-7 receptor alpha chain precursor (IL-7R-alpha) (CDW127)
DE (CD127 antigen).
GN IL2R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=90199875; PubMed=2317865;
RA Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A.,
RA Gimble S., Cosman D., Dower S.K., March C.J., Naman A.E., Park L.S.;
RT "Cloning of the human and murine interleukin-7 receptors:
RT demonstration of a soluble form and homology to a new receptor
RT superfamily.";
RL Cell 60:941-951(1990).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-7.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND ALSO SECRETED.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: H20 (SHOWN HERE), H1 AND
CC H6/SECRETED; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD127 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd127.htm".
CC -----
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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M29696; AAA59157.1; .

DR PIR; A34791; A34791.

DR PIR; B34791; B34791.

DR PIR; C34791; C34791.

DR MIM; 14661; .

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR003531; Hematopo_receptor_S_F1.

DR Pfam; PF00041; fn3; 1.

DR Prosite; PS01355; HEMATOPO_REC_S_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
Phosphorylation.

FT SIGNAL 1 20

FT CHAIN 21 459 INTERLEUKIN-7 RECEPTOR ALPHA CHAIN.

FT DOMAIN 21 239 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 240 264 POTENTIAL.

FT DOMAIN 265 459 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 128 224 FIBRONECTIN TYPE-III.

FT DOMAIN 184 189 SER/THR-RICH.

FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT MOD_RES 282 282 PHOSPHORYLATION (BY PKC) (POTENTIAL).

FT VARSPLIC 237 459 EMDPILITISLISFSAVALLVILACYLKKRIKPIYPSLP

FT DHKRTLEHLCKPKRLNVSFNPESFLDCQIHKRVDDIQARD

FT EVEGFLDTPPOOLESEKORLGGDQSPNCPSEDDVYVPE

FT SFGRDSSLTCLAGNVSACDAPILSSRSILDCRESGKNGPHV

FT YODLLSLGTNSTLPPPSLOSIGILTLPVAGOPILSL

FT GSNQEEAYVTMSSEFYONO -> LSLSTGVPSPILRLNMF

FT VRLNQEKI (IN ISOFORM H6).

FT NLNVSFNPESFLDCQIHRYDDIQARDEVEGFLDTPPOOLE

FT ESEKORLGGDQSPNCPSEDDVYVPEFGRDSSLTCLAGNVS

FT SACDAPILSSRSILDCRESGKNGPHYODLLSLGTNSTL

FT PPFSLOSIGILTLPVAGOPILSLGNSQEEAYVTMSSEFY

FT ONO -> VSVFGA (IN ISOFORM H1).

SO SEQUENCE 459 AA; 51566 MW; 0FDF4C84481BBB38 CRC64;

Query Match 10.3%; Score 123; DB 1; Length 459;
Best Local Similarity 20.3%; Pred. No. 0.0013;
Matches 42; Conservative 41; Mismatches 74; Indels 50; Gaps 8;

38 ELKDEATSCSLHRSANHATHATTC-----HMDVFH 68

34 ELDDYSFSCYSQLEVNGSOH-SLTCAFEEDPDVNTNLEFEICGALVEVKCLNFRKLOEIT 92

69 FMADDFISV-----NITDOSGNSOEGCSFLASIKRAPPENVTYTF---SGOYNISWRS 121

93 FIFTKKFLITGKSNICVKVEKSLTCKKIDLTIVKPEAPFDLSVIYREGANDFVYTFNT 152

122 DYEDPAFYMLKGLQYELQYRNRGD--PMAVSPRRKLISVDSRSVSLPLLEFRKSSYEL 179

153 SHLOKKYVVKV---LMDVAVYRQEKDENKWT-----HVNLSSTKLTLLQKRLQPAAMYEI 203

180 QVRAGPMPGSSSYGTWSEWSDPIVFOF 206

204 KVRSS--IPDHYFKGFSEWSPSYTFRT 228

Search completed: June 28, 2002, 07:43:20
Job time: 155 sec

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QY 61 TCHADVHFHMADDIFSVNITDQSGNYSOBGCSFLLAESIKRAPPENVTYTFSGOYNISMR 120
DB 80 TCHADVHFHMADDIFSVNITDQSGNYSOBGCSFLLAESIKRAPPENVTYTFSGOYNISMR 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLPEFRKDSYELQ 180
DB 140 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLPEFRKDSYELQ 199
QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 218
DB 200 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 237

RESULT 2
US-09-522-217-115
; Sequence 115, Application US/09522217
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYDTQVTCILEMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 60
DB 20 CPDLVCTDYDTQVTCILEMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 79
QY 61 TCHADVHFHMADDIFSVNITDQSGNYSOBGCSFLLAESIKRAPPENVTYTFSGOYNISMR 120
DB 80 TCHADVHFHMADDIFSVNITDQSGNYSOBGCSFLLAESIKRAPPENVTYTFSGOYNISMR 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLPEFRKDSYELQ 180
DB 140 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLPEFRKDSYELQ 199
QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 218
DB 200 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 237

RESULT 3
US-09-522-217-97
; Sequence 97, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
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APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Sprecher, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalalpha1 soluble receptor polypeptide sequence
US-09-522-217-97

Query Match 100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYDTQVTCILEMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 60
DB 389 CPDLVCTDYDTQVTCILEMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 448
QY 61 TCHADVHFHMADDIFSVNITDQSGNYSOBGCSFLLAESIKRAPPENVTYTFSGOYNISMR 120
DB 449 TCHADVHFHMADDIFSVNITDQSGNYSOBGCSFLLAESIKRAPPENVTYTFSGOYNISMR 508
QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLPEFRKDSYELQ 180
DB 509 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLPEFRKDSYELQ 568
QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 218
DB 569 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 606

RESULT 4
US-08-599-455B-2
; Sequence 2, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:41:41 ; Search time 43.94 Seconds

(without alignments)
90.053 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850
Sequence: 1 MRSSPGNMRIYICLMTYFL.....LQKMTIHQLSSRTGSEDS 162

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA.*

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	4	US-09-522-217-2
2	695.5	81.8	519	4	US-09-522-217-85
3	486	57.2	146	4	US-09-522-217-56
4	394	46.4	510	4	US-09-522-217-89
5	212	24.9	40	4	US-09-522-217-72
6	176	20.7	32	4	US-09-522-217-73
7	99.5	11.7	114	1	US-08-031-399-6
8	99.5	11.7	114	1	US-08-031-399-12
9	99.5	11.7	114	1	US-08-393-305-3
10	99.5	11.7	114	1	US-08-726-817-3
11	99.5	11.7	114	1	US-08-504-042-6
12	99.5	11.7	114	1	US-08-504-042-12
13	99.5	11.7	114	2	US-08-725-969-3
14	99.5	11.7	114	2	US-08-794-524-3
15	99.5	11.7	114	4	US-09-189-193-3
16	99.5	11.7	114	5	PCT-US94-03793-6
17	99.5	11.7	114	5	PCT-US94-03793-12
18	99.5	11.7	162	1	US-08-031-399-5
19	99.5	11.7	162	1	US-08-393-305-2
20	99.5	11.7	162	1	US-08-535-733-2
21	99.5	11.7	162	1	US-08-726-817-2
22	99.5	11.7	162	1	US-08-504-042-5
23	99.5	11.7	162	1	US-08-725-969-2
24	99.5	11.7	162	2	US-08-794-524-2
25	99.5	11.7	162	3	US-08-842-947-6
26	99.5	11.7	162	4	US-09-189-193-2
27	99.5	11.7	162	4	US-09-522-217-113

28	99.5	11.7	162	5	PCT-US94-03793-5	Sequence 5, Appl1
29	99.5	11.7	162	5	PCT-US96-06423-2	Sequence 2, Appl1
30	94.5	11.1	114	1	US-08-031-399-3	Sequence 3, Appl1
31	94.5	11.1	114	1	US-08-393-305-6	Sequence 6, Appl1
32	94.5	11.1	114	1	US-08-726-817-6	Sequence 6, Appl1
33	94.5	11.1	114	1	US-08-504-042-3	Sequence 3, Appl1
34	94.5	11.1	114	2	US-08-725-969-6	Sequence 6, Appl1
35	94.5	11.1	114	2	US-08-794-524-6	Sequence 6, Appl1
36	94.5	11.1	114	4	US-09-189-193-6	Sequence 6, Appl1
37	94.5	11.1	114	5	PCT-US94-03793-3	Sequence 3, Appl1
38	94.5	11.1	122	1	US-08-300-903A-3	Sequence 3, Appl1
39	94.5	11.1	162	1	US-08-031-399-2	Sequence 2, Appl1
40	94.5	11.1	162	1	US-08-393-305-5	Sequence 5, Appl1
41	94.5	11.1	162	1	US-08-284-393B-9	Sequence 9, Appl1
42	94.5	11.1	162	1	US-08-726-817-5	Sequence 5, Appl1
43	94.5	11.1	162	1	US-08-504-042-2	Sequence 2, Appl1
44	94.5	11.1	162	2	US-08-725-969-5	Sequence 5, Appl1
45	94.5	11.1	162	2	US-08-794-524-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-522-217-2
Sequence 2, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C. ?
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OR INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
EARLIER FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.8e-87;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMRIYICLMTYFLGTLVHKSSGODRHMTIRMQLDIYDQKNVNDLVPF 60
DB 1 MRSSPGNMRIYICLMTYFLGTLVHKSSGODRHMTIRMQLDIYDQKNVNDLVPF 60
QY 61 LPAPDEVETNCWSAFSCFOKAOLKSANTGNERRIIVNSIKIKRPPSTNAGROKRL 120
DB 61 LPAPDEVETNCWSAFSCFOKAOLKSANTGNERRIIVNSIKIKRPPSTNAGROKRL 120
QY 121 TPCSDSYKKPKPELEFRKSLQKMIHQLSSRTGSEDS 162
DB 121 TPCSDSYKKPKPELEFRKSLQKMIHQLSSRTGSEDS 162

in particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft versus host disease, disorders involving the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney disorders including polycystic kidney disease, cystic renal dysplasia, disorders of the thymus including lymphomas, Hodgkin disease and carcinoids. The 16445 polypeptides are also useful as modulating agents in cellular processes including growth promoting activity, particularly the antigen-independent proliferation of T-helper cell clones. The encoding nucleic acid is useful as primers or hybridization probes for the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for tissue typing and in forensic biology. The present sequence represents the human IL-9/IL-2 receptor-like polypeptide (AAH16445).

Sequence 538 AA:

Query Match 100.0%; Score 1195; DB 22; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYLYQVTCILEMNLHPSTLTWQDQYELKDEATSCSLHRAHNAHTATY 60
|||||
20 cpdlvctdylyqvtvcllemnlhpsltltwqdyelkdeatscslhrahnahtaty 79

61 TCHMDVHFMAADIFSVNTTDSQNGVSOEGSFLLAESIKRPAPPNVTVPSGOYNISMR 120
|||||
80 tchmdvfhmaddifsvnttdsgngvsgcgsfllaesikrpapfnvrvtsqynlswr 139

121 SDYEDPAFYMLKGLQYELQYRNKGDPMVAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
|||||
140 sdyedpafymkglqyelyqrnrgdpmavsprrklisvdsrsvsllplefrkdsyelyq 199

181 VRAGPMPGSSYOGTSEWSDPYIFOTOSELEKEGNPH 218
|||||
200 vragpmpgssyogtsewsdpyifqtgeelkegnph 237

RESULT 9
ID AAB18629
ID AAB18629 standard; Protein: 606 AA.

AA18629;
22-JAN-2001 (first entry)

Amino acid sequence of MBP-human zalphall ligand fusion.
zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma; tumorigenesis; leukemia; hematopoiesis; B cell tumour.

Synthetic.
Homo sapiens.

WO200053761-A2.

14-SEP-2000.

09-MAR-2000 / 2000WO-US06067.

09-MAR-1999; 99US-0264908.
11-MAR-1999; 99US-0265992.
01-JUL-1999; 99US-0142013.

(ZYMO) ZYMOGENETICS INC.

Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

WPI: 2000-565600/52.
K-PSDB: AAA75609.

PT New human cytokine, designated zalphall ligand, useful for stimulating

the proliferation and/or development of haematopoietic cells in vitro and in vivo, and for treating tumourigenesis -
Example 45; Page 245-247; 256pp; English.

The present sequence represents a MBP-human zalphall ligand fusion. Zalphall ligand is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haematopoietic cells in vitro and in vivo. Zalphall ligand polynucleotides can be used as primers or probes for cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, CC polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand genetic defect.

Sequence 606 AA:

Query Match 100.0%; Score 1195; DB 21; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYLYQVTCILEMNLHPSTLTWQDQYELKDEATSCSLHRAHNAHTATY 60
|||||
389 cpdlvctdylyqvtvcllemnlhpsltltwqdyelkdeatscslhrahnahtaty 448

61 TCHMDVHFMAADIFSVNTTDSQNGVSOEGSFLLAESIKRPAPPNVTVPSGOYNISMR 120
|||||
449 tchmdvfhmaddifsvnttdsgngvsgcgsfllaesikrpapfnvrvtsqynlswr 508

121 SDYEDPAFYMLKGLQYELQYRNKGDPMVAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
|||||
509 sdyedpafymkglqyelyqrnrgdpmavsprrklisvdsrsvsllplefrkdsyelyq 568

181 VRAGPMPGSSYOGTSEWSDPYIFOTOSELEKEGNPH 218
|||||
569 vragpmpgssyogtsewsdpyifqtgeelkegnph 606

RESULT 10
ID AAY79316
ID AAY79316 standard; Protein: 606 AA.

AA79316;

18-JUL-2000 (first entry)

Maltose binding protein-zalphall fusion protein.

Cytokine receptor; zalphall; maltose binding protein; human; apoptosis; signal transduction; growth factor; cancer; tumour; infection; gene therapy; diagnosis; muzalphall/MBP-6H.

Homo sapiens.

Key Location/Qualifiers

Protein 1..388 "maltose binding protein"

Protein 389..606 /note="zalphall cytokine binding domain"

WO200017235-A2.

30-MAR-2000.
23-SEP-1999; 99WO-US22149.

XX 23-SEP-1998; 98US-0159254.
 PR 09-MAR-1999; 99US-0265117.
 PR 06-JUL-1999; 99US-0347930.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 XX Presnell SR, Conklin DC, Novak JE, Hammond AF;
 PI
 XX WPI: 2000-292825/25.
 DR N-PSDB; AA294554.
 XX
 PT Novel nucleic acid encoding zalpahal polypeptide, useful for treating
 PT e.g. viral infection or tumors, and for identifying ligands that
 PT stimulate cell proliferation
 XX
 PS Example 13; Page 166-168; 190pp; English.

The present sequence is that of a fusion protein, designated huzalpalhal/MBP-6H, comprising a maltose binding protein (MBP) fused to the cytokine binding domain (amino acids 20-237) of human class I cytokine receptor zalpahal (see AA79312). An expression plasmid containing huzalpalhal/MBP-6H DNA (see AA294554) was constructed via homologous recombination and the fusion protein CC was expressed in Escherichia coli BL21 using vector plasmid pTAP98. CC cell signalling molecule, growth factor receptor, or is a CC extracellular matrix associated protein with growth factor hormone CC activity. The invention provides zalpahal polypeptides (including CC fusion proteins), polynucleotides and antibodies, and methods for CC their use in the treatment and diagnosis of conditions associated CC with altered zalpahal expression or activity.

XX Sequence 606 AA;

Query Match 100.0%; Score 1195; DB 21; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVYICILEMNLHPSTLTLTWQDYELKDEATSCSLHRSANHATATY 60
 DB 389 cpdlvctdylytvtcllemwnlhpstltltwqdyeelkdeatcsclhrahathaty 448
 QY 61 TCHMDVFHMDADIFSVNTDQSGNYSGEGSFLLAESIKPAPFNVTWTFSGQYINSMR 120
 DB 449 tchmdvfhmaddifsvntdsgnysgegsfllaesikpappfnvltvsgqynlswr 508
 QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPWAVSPRRKLISVDSRVSLLPLEFRKDSYELQ 180
 DB 509 sdyedpatfymkglqyelqyrnrgdpwavsprkrlisvdsrsvsllplefrkdsyeld 568
 QY 181 VRAGPMGSSYOGTWSMSDPVIFQTOSEELKEGWNPH 218
 DB 569 vragpmpgssyqgtwsewdpvlftqseelkegwnph 606

RESULT 11

AA794304
 ID AA794304 standard; Protein: 538 AA.

XX AA794304;

XX 08-AUG-2000 (first entry)

DE Human HNOVILR polypeptide 1.

XX Human; anticancer; anti-inflammatory; immunosuppressive; anti-allergic;
 KM antiasthmatic; antirheumatic; antiarthritic; nootropic; vasotropic;
 KM neuroprotective; antibacterial; cerebroprotective; osteopathic;
 KM nephrotoxic; hepatotoxic; hypotensive; hypertensive; antifungal;
 KM anti-HIV; antiprotocan; antiviral; antianemic; autoimmune disease;
 KM Crohn's disease; Alzheimer's disease; Parkinson's disease; stroke;

KM multiple sclerosis; cancer; infection; cardiovascular disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200027882-A1.
 PN
 XX 18-MAY-2000.
 PD

XX 01-NOV-1999; 99WO-US25617.

XX 06-NOV-1998; 98US-0187711.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX Kikly KR, Michalovich D;

XX WPI: 2000-376497/32.

XX N-PSDB; AA26984.

PT Isolated polypeptide of HNOVILR type used for diagnosing or treating
 PT for example cancer, inflammation, autoimmune disease -
 XX
 XX Claim 1; Page 30-31; 36pp; English.

The present sequence is a HNOVILR polypeptide which is believed to be a member of the cytokine receptor family of polypeptides. It shows homology with human interleukin receptor 2 and is therefore expected to have similar biological functions/properties. The polynucleotide may be obtained from a cDNA library derived from mRNA in cells of human bone marrow using expressed sequence tag (EST) analysis. Alternatively it can be synthesised from natural sources such as genomic DNA libraries or CC can be synthesised using commercially available techniques. The growth, CC regulation and functional activities of cells are regulated through the CC interaction of cytokines and their cognate receptors. Thus the CC gene sequence and its product are useful for diagnosing or treating a CC wide range of diseases including cancer, inflammation, autoimmune disease, Crohn's disease, allergy, asthma, rheumatoid arthritis, CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, CC head injury damage, septic shock, stroke, osteoporosis, osteoarthritis, CC cardiovascular disease, kidney disease, liver disease, ischemic injury, CC myocardial infarction, hypotension, hypertension, acquired immune CC deficiency syndrome (AIDS), male pattern baldness, and bacterial, CC fungal, protozoan and viral infections.

SO Sequence 538 AA;

Query Match 99.4%; Score 1188; DB 21; Length 538;
 Best Local Similarity 99.5%; Pred. No. 8.5e-115;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVYICILEMNLHPSTLTLTWQDYELKDEATSCSLHRSANHATATY 60
 DB 20 cpdlvctdylytvtcllemwnlhpstltltwqdyeelkdeatcsclhrahathaty 79
 QY 61 TCHMDVFHMDADIFSVNTDQSGNYSGEGSFLLAESIKPAPFNVTWTFSGQYINSMR 120
 DB 80 tchmdvfhmaddifsvntdsgnysgegsfllaesikpappfnvltvsgqynlswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPWAVSPRRKLISVDSRVSLLPLEFRKDSYELQ 180
 DB 140 sdyedpatfymkglqyelqyrnrgdpwavsprkrlisvdsrsvsllplefrkdsyeld 199
 QY 181 VRAGPMGSSYOGTWSMSDPVIFQTOSEELKEGWNPH 218
 DB 200 vragpmpgssyqgtwsewdpvlftqseelkegwnph 237

RESULT 12

AA008728
 ID AA008728 standard; Protein: 538 AA.

XX AA008728;

Query Match 100.0%; Score 1195; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.2e-110;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTYLQVVICILEMNNLHPSTLTLTWODYEEELKDEATSCSLHRSANATHARY 60
 DB 20 CPDLVCYTYLQVVICILEMNNLHPSTLTLTWODYEEELKDEATSCSLHRSANATHARY 79
 QY 61 TCHMDVHFHMADDFSVNTTDSGNSQECGFLAESIKPAPFNVTVTFSGOYNISMR 120
 DB 80 TCHMDVHFHMADDFSVNTTDSGNSQECGFLAESIKPAPFNVTVTFSGOYNISMR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 199
 QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQSEBELKEGNMPH 218
 DB 200 VRAGPMPGSSYOGTWSWSDPVIFOTQSEBELKEGNMPH 237

SULT 2
 DB91
 ID 09HB91 PRELIMINARY; PRT: 538 AA.
 AC 09HB91;
 DT 01-MAR-2001 (TREMBLrel, 16, Created)
 DT 01-JUN-2001 (TREMBLrel, 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)
 DE NOVEL INTERLEUKIN RECEPTOR.
 GN NLR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20481926; PubMed=11016959;
 RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
 RT "Cloning of a type I cytokine receptor most related to the IL-2
 RT receptor beta chain."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
 DR EMBL: AF269133; AAC23419.1; -.
 DR EMBL: AF269134; AAC23420.1; -.
 DR InterPro: IPR003961; FN.LII.
 DR SMART: SM00060; FN3; I.
 KW Receptor.
 SQ SEQUENCE 538 AA; 59228 MW; 23D7F3EDFC74915B CRC64;

Query Match 100.0%; Score 1195; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.2e-110;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-OCT-2000 (TREMBLrel, 15, Created)
 DT 01-OCT-2000 (TREMBLrel, 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)
 DE LYMPHOCYTE RECEPTOR BETA (INTERLEUKIN 21 RECEPTOR) (NOVEL INTERLEUKIN
 DE RECEPTOR).
 GN LR-BETA OR IL21R OR NLR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finnelly H.,
 RA Dardigian C., Lowe L., Wood C.R., Young D.A., Collins M.;
 RT "Chromosome 16p12 Encodes a Biologically Active IL-2RB Related
 RT Receptor with Lymphoid Restricted Expression."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=20531754; PubMed=11081504;
 RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
 RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
 RA Burkhead S., Hejblum M., Brandt C., Kuilper J.L., Kiemer J.,
 RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
 RA Mudri S., Clegg C., Moore M., Grant F., Lofton-Day C., Gilbert T.,
 RA Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
 RA Maurer M., Kausansky K., Holly R.D., Foster D.;
 RT "Interleukin 21 and its receptor are involved in NK cell expansion and
 RT regulation of lymphocyte function."
 RL Nature 408:57-63(2000).
 RN [3]
 RP TISSUE=THYMUS, AND SPLEEN.
 RC SEQUENCE FROM N.A.
 RX MEDLINE=20481926; PubMed=11016959;
 RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
 RT "Cloning of a type I cytokine receptor most related to the IL-2
 RT receptor beta chain."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
 DR EMBL: AF279436; AAF86350.1; -.
 DR EMBL: AF254068; AAC29347.1; -.
 DR EMBL: AF269134; AAC23420.1; -.
 DR MGD: MGI:1890475; 1121r.
 KW Receptor.
 SQ SEQUENCE 529 AA; 58354 MW; 8B41816B80D426581 CRC64;

Query Match 70.6%; Score 844; DB 11; Length 529;
 Best Local Similarity 69.3%; Pred. No. 1.1e-75;
 Matches 151; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

QY 1 CPDLVCYTYLQVVICILEMNNLHPSTLTLTWODYEEELKDEATSCSLHRSANATHARY 60
 DB 20 CLDICTCTDYLTTCVLETRSPNPSTLSTWODEYELDDOETFCGLHSGNTHIHW 79
 QY 61 TCHMDVHFHMADDFSVNTTDSGNSQECGFLAESIKPAPFNVTVTFSGOYNISMR 120
 DB 80 TCHMDVHFHMADDFSVNTTDSGNSQECGFLAESIKPAPFNVTVTFSGOYNISMR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180
 DB 140 SAYDEPSNYVLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 199
 QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQSEBELKEGNMPH 218
 DB 200 VRAPQPTSTRTGTSWSDPVIFOTQAGRPACMDPH 237

RESULT 4
 ID 09ESM1 PRELIMINARY; PRT: 529 AA.
 AC 09ESM1;
 DT 01-MAR-2001 (TREMBLrel, 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE NOVEL CYTOKINE RECEPTOR NR8.
 GN IL2IR OR NR8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/C;
 RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
 RT "A novel cytokine receptor NR8 is closely mapped to IL-4R:
 RT Polymorphism in Balb/c mouse.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045137; BAB13736.1; -.
 DR MGI: 1890475; 1121r.
 DR InterPro: IPR003961; FN_III.
 DR SMART: SM00060; FN3; 1.
 SO RECEPTOR.
 SQ SEQUENCE 529 AA: 58358 MW: 212834822AA7722B CRC64;

Query Match 70.1%; Score 838; DB 11; Length 529;
 Best Local Similarity 68.3%; Pred. No. 4.5e-75;
 Matches 149; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

QY 1 CDLVCTTYLTQVTCILEMNNLHPSTLTTLTWQDOYEELKDEATSCSLHRSANHTATY 60
 DB 20 CDLVCTTYLTQVTCILEMNNLHPSTLTTLTWQDOYEELKDEATSCSLHRSANHTATY 79
 QY 61 TCHMDVFHMAADDIFSVNTIDSGNYSQEGSFLAESIKPAPNNVTFESGQYINSMR 120
 DB 80 TCHMRISQFLSDSEVFLVNTIDSGNNSQEGSFLAESIKPAPNNVTFESGQYINSMR 139
 QY 121 SYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSKSVSLPLEERKDSYELQ 180
 DB 140 SADEPSNYYLVLRKQLQYELQYRNKGDPMVSPRRKLISVDSKSVSLPLEERKDSYELQ 199
 QY 181 VRAGPMGSSYOGTSEMSDPIYFOTQSELEKEGNPH 218
 DB 200 MRAAPQGTSPFRGTSEMSDPIYFOTQSELEKEGNPH 237

RESULT 5
 Q64146 PRELIMINARY; PRT; 896 AA.

Q64146: 064146:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
 GN IL-3R<BETA>.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95370942; PubMed=7643220;
 RA Appel K., Butlini M., Sauter A., Gebicke-Haerter P.J.;
 RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
 RT microglia and its mRNA expression in vivo.";
 RL J. Neurosci. 15:5800-5809(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISTAR; TISSUE=BRAIN;
 RA Gebicke-Haerter P.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: S79263; AAB35068.1; -.
 DR EMBL: A400055; CAA04186.1; -.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR000282; Cytok_receptor_2.

DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_FL.
 DR Pfam: PFC0041; FN3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01355; HEMATOPO_REC_S_FL; UNKNOWN_1.
 KW Signal.
 FT NON_TER 1 1
 FT NON_TER 896 896
 SQ SEQUENCE 896 AA: 99504 MW: 4C6E3B288A4A1052 CRC64;

Query Match 13.6%; Score 162.5; DB 11; Length 896;
 Best Local Similarity 26.5%; Pred. No. 1.7e-07;
 Matches 59; Conservative 32; Mismatches 89; Indels 55; Gaps 9;

QY 4 LVCYTDYLTQVTCILEMNNLHPSTLTTLTWQDOYEELKDEATSCSL----- 48
 DB 37 LVCYNDYIERILCSWADTEDAGLVNLTLYHWD-----VKQAQVQPPPP 91
 QY 49 HRSANHTATY-----CHMDVFHMAADDIFSVNTIDSGNYSQEGSFLAESIKPAP 104
 DB 92 HRCVPRRCVLPYTFQSVSKEDYSLQPDRLSTHLV-----VPLAQVQPPPP 139
 QY 105 FNYTFESG-QYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSR 162
 DB 140 KDLSISPSGDHFLKMSVPLGDAQVSLSGKDQIFEVAYKQIQDSWE-----DAS 189
 QY 163 S-----VSLPLEERKDSYELQYRNKGDPMVSPRRKLISVDSR 210
 DB 190 SLTCHMLMTLEPKLPLPNSIYAVRAQLAPGSSLSGRPSGMSPEVHMDSPTE 244

RESULT 6
 Q921A0 PRELIMINARY; PRT; 890 AA.

Q921A0: 0921A0:
 AC Q921A0;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
 GN IL5.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Logsdon N.J., Graham A., Scott C.W.;
 RT "Guinea pig IL5 receptor beta chain.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U94688; AAC77520.1; -.
 DR HSSP: P40189; 1BQV.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_FL.
 DR Pfam: PFC0041; FN3; 3.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01355; HEMATOPO_REC_S_FL; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 890 AA: 96579 MW: D43FB1CA8852536 CRC64;

Query Match 13.0%; Score 155.5; DB 11; Length 890;
 Best Local Similarity 26.5%; Pred. No. 8.6e-07;
 Matches 57; Conservative 33; Mismatches 78; Indels 47; Gaps 10;

QY 3 DLVCYTDYLTQVTCILEMNNLHPSTLTTLTWQDOYEELKDEATSCSL----- 46
 DB 250 NLQCVFPGATILSCSMVRSQVTSVSGFLFYSSLDAGEQCPQVQKELHDITRSC 309
 QY 47 SLHRSANHTATYTCMDVFHMAADDIFSVNTIDSGNYSQEGSFLAESIKPAP 105
 DB 310 QI-RVSNPRHSQY-----VTVPRNGEKIRSANHIQMA-----APTL 348

QY 106 NATVFSGQYINISMSRSDYEDPAFYMLKGLQYELQYRNKGDPAVSPRRKLISYDSRSVS 165
 DB 349 NVTKD-GDYSLRWYET-----KMYSHIENTFEIQYRRAGDMENSKETL--KNAHMP 401
 QY 166 LPLFRKDSYELQYRAGPMGSSYQGTWSEMSD 200
 DB 402 LPPLE--PATTYLAIRVVRKPGGAYNGIWMSE 434

RESULT 7
 ID Q90MG3 PRELIMINARY; PRT; 1162 AA.
 AC Q90MG3;
 DT 01-MAY-2000 (Tremblrel, 13, Created)
 DT 01-MAY-2000 (Tremblrel, 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
 DE LEPTIN RECEPTOR B.
 GN LEPR OR LEPRB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-KK OBES; TISSUE-BRAIN, HYPOTHALAMUS;
 RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
 RA Joost H.G.;
 RT "hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
 RT hyperinsulinemic KK mouse strain."
 RL J. Endocrinol. 21:337-345(1998).
 DR EMBL; Y10296; CA471342.1; -.
 DR HSSP; P16471; 1BP3.
 DR MGD; MG1:104993; Lepr.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 3.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 FT VARIANT 600 N -> D.
 SQ SEQUENCE 1162 AA; 130787 MW; 541E77CBB46EC00D CRC64;

Query Match 12.1%; Score 144; DB 11; Length 1162;
 Best Local Similarity 31.1%; Pred. No. 1.7e-05;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

DB 39 LKDE-----ATSCLSRHSANATHATYCHMDVFH-----FMADDIFSVNITDQSGNTS 87
 DB 177 LKDSFQTVQNCISLRGC-----ECHVPPRAKLNALMLYLETISAGVSFQSPILMS 227
 QY 88 QECGSLFLASIKRPAP--FNVTYFSGQYINISMSRSDYEDPAFYMLKGLQYELQYRNNG 145
 DB 228 LQ--PMYV---VKPDPPLGLRMEVTDGNTKISWDSQTNAF-----PLQYQVYKLEMS 276
 QY 146 DPMAVSPRRKLISYDSRSV-SLPLFRKDSYELQYRAGPMGSSYQGTWSEMSDPIYF 204
 DB 277 T--IVREAETVSVATSLVDVSLP-----GSSYEQVRSKRILDS--GWSWDSMPQV 326
 QY 205 QTO 207
 DB 327 TTD 329

RESULT 8
 ID Q62960 PRELIMINARY; PRT; 895 AA.
 AC Q62960;
 DT 01-NOV-1996 (Tremblrel, 01, Created)

DT 01-NOV-1996 (Tremblrel, 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
 DE LEPTIN RECEPTOR.
 GN ROB-R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RA Wang M.-Y., Unger R.H.;
 RT "Characterization of leptin receptors in normal and Zucker diabetic
 RT fatty rats."
 RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U53144; AB03088.1; -.
 DR HSSP; P16471; 1BP3.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737C07 CRC64;

Query Match 11.5%; Score 138; DB 11; Length 895;
 Best Local Similarity 30.9%; Pred. No. 4.8e-05;
 Matches 56; Conservative 23; Mismatches 62; Indels 40; Gaps 11;

QY 39 LKD--EATSCLSRHSANATHATYCHMDVFH-----FMADDIFSVNITDQSGNTS 89
 DB 177 LKDSFQTVQNCISLRGC-----NCSVRECECHVPPRAKVNVALMLYLETISAGVSFQSPILMS 229
 QY 90 CGSLFLASIKRPAP--FNVTYFSGQYINISMSRSDYEDPAFYMLKGLQYELQYRNNDP 147
 DB 230 --PMYV---VKPDPPLGLRMEVTDGNTKISWDSQTNAF-----PLQYQVYKLEMS 277
 QY 148 WAVSPRRKLISYDSRSV-SLPLFRKDSYELQYRAGPMGSSYQGTWSEMSDPIYFOT 206
 DB 278 -IVREAETVSVATSLVDVSLP-----GSSYEQVRSKRILDS--GWSWDSMPQLFTT 328
 QY 207 Q 207
 DB 329 Q 329

RESULT 9
 ID Q92919 PRELIMINARY; PRT; 896 AA.
 AC Q92919;
 DT 01-FEB-1997 (Tremblrel, 02, Created)
 DT 01-FEB-1997 (Tremblrel, 02, Last sequence update)
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
 DE LEPTIN RECEPTOR.
 GN DB.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
 RA Matthews W.;
 RL Curr. Biol. 6:0-0(0).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97215244; PubMed=9061609;
 RA Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;

RT "Cloning and characterization of a human leptin receptor using a
RT biologically active leptin immunoadhesin.",
RL J. Mol. Endocrinol. 18:77-85(1997).
DR EMBL: U66495; AAB07495.1; -.
DR EMBL: U50748; AAC26350.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3_2.
DR SMART: SM00060; FN3_1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
SQ SEQUENCE 896 AA; 102489 MW; D31C7AA4186DEB3 CRC64;

	Query Meth.	11.5%;	Score 137;	DB 4;	Length 896;
	Best Local Similarity	28.0%;	Pred. NO. 6e-05;		
	Matches 47;	Conservative	Mismatches 68;	Indels 28;	Caps
OY	45 SCSLHRSANHATATATCTCHMDVFHFMADD--ITSVNITDQSGNYSQEGSFLLESTKIPA 102				
Db	187 NCSEVHECC-----CLVPYPRAKLNDPLMLCKLTETSGVIFGSPMSVGPIMMYKD 238	:::: :	:	: :	:
OY	103 PP--FNVTYTFSGQINISMRSDYEDPAFTMIKGKLOLETQIRNRGDPMNAVSEFRKKLSVD 160	:::	:	:	:
Db	239 PRLGLMELTIDGDNLKISWSP-----PLTPFPLOYOKY--SENSTVIAREADIKVSAT 291	:::	:	:	:
OY	161 SRSY-SLLPLEPRKDSVELYORAGPMPGSSYGOTSEMWDPIPTQO 207	:	:	:	:
Db	292 SLAVDSLTP-----GSSEIVQKRGRLLDG--PCJMSDMSTPVPFVTTQ 331	:	:	:	:

RESULT	10			
Q92920				
ID	Q92920	PRELIMINARY:	PRT:	958 AA.
AC	Q92920;			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	LEPTIN RECEPTOR.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid:9606;			
PN	[1]			
PP	SEQUENCE FROM N.A.			
RX	MEDLINE-6638968; PubMed-8805376;			
RA	Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,			
RA	Mathews W.;			
RT	"A role for leptin and its cognate receptor in hematopoiesis.";			
RL	Curr. Biol. 6:1170-1180(1996).			
DR	EMBL; U66496; AB07496.1; -.			
DR	HSSP; P16471; 1BP3.			
DR	InterPro: IPR002966; CR1A.			
DR	InterPro: IPR003966; FN1111.			
DR	InterPro: IPR003529; Hematopo_receptor_L_F2.			
DR	InterPro: IPR003531; Hematopo_receptor_S_F1.			
DR	Pfam; PF00041; fn3; 2.			
DR	SMART; SM00060; FN3; 1.			
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN1.			
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN1.			
KW	Receptor.			
SQ	SEQUENCE 958 AA; 109392 MW; 3F65FC5A187E803A CRC64;			

	Query Match	11.5%	Score 137	DB 4	Length 958
	Best Local Similarity	28.0%	Prod. No. 6.5e-05		
	Matches 47	Conservative 25	Mismatches 68	Indels 28	Gaps
QY	45	SCSHRSANHATATATCTCMDFVHFHMADD--IFSVNTIDDSGMYSGECSFLIASIKPA	100		
			: :	:	:

```
Dbb      187 NCSVHECC-----CLVPPTAKLIDMLMLKLTSGGVAFOSPLMSVQPIIMXKPD 236d
Oy       103 PP--FNTVFYFGGYNIIMSRSDEDPARYMLKGLEYELDYNRGPMPAVSRRLLISVD 160d
Db        239 PLGLHMEITDDONLKISMSP-----PLVPPFLQYQVK-SENVTVIREADKIYSAT 291d
Oy        161 SRSY-SILPTEFRKDSYSTLOYRAGPMRGSSYGCTGSEWSDPIRFTQ 207d
Db        292 SLIVDSLTP----GSSTEVQYGRGRLLDG---PSIMSDMSTPVPVFTIQ 331d
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Q92921			
ID	Q92921	PRELIMINARY;	PRT: 1165 AA.
AC	Q92921;		
DT	01-FEB-1997 (TREMBLrel. 02, Created)		
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)		
DE	1l-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	LEPTIN RECEPTOR.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=6638968; PubMed=6805376;		
RA	Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,		
RA	Matthews W.;		
RT	"A role for leptin and its cognate receptor in hematopoiesis";		
RL	Curr. Biol. 6:1170-1180(1996).		
DR	EMBL; U66497; AAB07497.1; -		
DR	HSSP; P16471; 1BP3.		
DR	InterPro; IPR002926; CRA.		
DR	InterPro; IPR003961; FN_III.		
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.		
DR	InterPro; IPR003531; Hematopo_receptor_S_F1.		
DR	Pfam; PF00041; fn3. 2.		
DR	SMART; SM00060; FN3. 1.		
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.		
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.		
KW	Receptor.		
SQ	SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;		

Query Match	11.5%;	Score 137;	DB 4;	Length 1165;
Best Local Similarity	28.0%;	Pred. No. 8.4e-05;		
Matches 47; Conservative	25;	Mismatches 68;	Indels 28;	Gaps 8;

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QY      45  SCSHRSANNAHTATYTCMDVDFHMADD--TFENVITDQSGVNSQCSGPLLASTESIPA 100
      111:::111:::111:::111:::111:::111:::111:::111:::111:::111:::111
Db      187  NCSVHECC-----CLVPYPTAKLNDITLMCLCKITSGVIFQSPMLNSVQPIMMVRPD 230
QY      103  PP--FNTVTFSGQYINMSRSDYEDPAATYMLKGLQYELQRRKQCPMAVSRRKLTISVD 160
      111:::111:::111:::111:::111:::111:::111:::111:::111:::111
Db      239  PFLCLHMETITDDNKLKIMSSP-----PLVPFLQIQVTK--SENSTYYIAREKDIKVSAT 290
QY      161  SRSY-SLLPLEFRKDSYELQYRAGPMGSSYQGTWSEMSDPVITFQTO 207
      111:::111:::111:::111:::111:::111:::111:::111:::111:::111
Db      292  SLVDLSILP-----GSSYEYQVGRKLUG--PGIWDMSWTSPKPVFTQ 331

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RESULT	12	
	Q13594	
ID	Q13594	PRELIMINARY;
AC	Q13594;	PRT; 896 AA.
DT	01-NOV-1996 (TIREMBLrel. 01, Created)	
DT	01-NOV-1996 (TIREMBLrel. 01, Last sequence update)	
DT	01-DEC-2001 (TIREMBLrel. 19, Last annotation update)	
DE	B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.	
OS	Homo sapiens (Human)	
CC	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
OX	NCBI_TaxID=9606;	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:42:52 ; Search time 65.65 seconds
(without alignments)
319,078 Million cell updates/sec

Title: US-09-825-561a-6

Sequence: 1 CPDLVCYTDYLTQTVICILEM.....SDPVIFQTSSELEKEGNPH 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162.5	13.6	876	1	I56563 interleukin-3 rece
2	145	12.1	878	2	A40091 interleukin-3 rece
3	144	12.1	805	2	S68441 lepin receptor, s
4	144	12.1	882	2	S68439 lepin receptor, s
5	144	12.1	894	2	S68437 lepin receptor, s
6	144	12.1	896	1	A35782 cytokine receptor
7	144	12.1	900	2	S68440 lepin receptor, s
8	144	12.1	1162	2	S68438 lepin receptor, s
9	141.5	11.8	539	2	A35052 interleukin-2 rece
10	139	11.6	579	2	B45266 MPL-K protein prec
11	139	11.6	635	2	A45266 MPL-K protein prec
12	138	11.5	895	2	S74225 lepin receptor, s
13	138	11.5	1162	2	PC4184 lepin receptor, O
14	135.5	11.3	825	1	A60386 interleukin-4 rece
15	134	11.2	537	2	B46535 interleukin-2 rece
16	133.5	11.2	369	2	I49280 interleukin-2 rece
17	132.5	11.1	625	2	S35317 hematopoietic grow
18	132.5	11.1	626	2	S37622 proto-oncogene - m
19	127	10.6	373	2	A55718 interleukin-2 rece
20	126	10.5	551	2	A30342 interleukin-2 rece
21	123	10.3	262	2	C34791 interleukin-7 rece
22	123	10.3	298	2	B34791 interleukin-7 rece
23	123	10.3	459	2	A34791 interleukin-7 rece
24	122	10.2	831	2	J01655 prolactin receptor
25	121.5	10.2	918	2	A44257 interleukin-6 sign
26	120	10.0	369	2	A44255 interleukin-2 rece
27	117	9.9	897	1	A39255 cytokine receptor
28	117	9.8	810	1	A33380 interleukin-4 rece
29	115	9.6	459	2	D34791 interleukin-7 rece

30	113.5	9.5	284	2	S27931 Env/v-mpl fusion p
31	113.5	9.5	800	1	S31575 interleukin-4 rece
32	112.5	9.4	917	2	I49699 glycoprotein 130 -
33	110.5	9.2	918	2	A36337 membrane glycoprot
34	108.5	9.1	468	1	A41242 interleukin-6 rece
35	106	8.9	638	2	S12136 interleukin-6 rece
36	105.5	8.8	279	2	B32985 somatotropin recep
37	105.5	8.8	440	2	JL0144 somatotropin-bndl
38	105.5	8.8	460	2	JL0145 interleukin-6 rece
39	105.5	8.8	638	2	A33505 somatotropin recep
40	105	8.8	522	2	B45268 interleukin-9 rece
41	104	8.7	638	2	B28176 somatotropin recep
42	103	8.6	508	1	ZUH0R erythropoietin rec
43	102	8.5	468	2	A45268 interleukin-9 rece
44	100.5	8.4	265	2	S14081 erythropoietin rec
45	99.5	8.3	507	1	A32385 erythropoietin rec

ALIGNMENTS

RESULT 1
I56563
Interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Butlini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GH/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:579263; NID:q1086954; PID:AA35068.1; PID:q1086955
C:Genetics:
A:Gene: rIL-3Rbeta
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 13.6% Score 162.5; DB 2; Length 896;
Best local Similarity 25.1% Pred. No. 2.3e-06;
Matches 59; Conservative 32; Mismatches 89; Indels 55; Gaps 9;

QY 4 LVGYNDYLTQTVICILEMNLHPSTLTLT--WDOYEELDEATCSL-----48
DB 37 LQCYNDYLTERTICSWADPEDAOGVNLTLVHMD-----KKQPMSCBLSHDLWSECPSS 91
QY 49 HRSANNAHATYT-----CHMDVFHMDADIRSVNITDQSGVSESGSFLAASIKAPP 104
DB 92 HNCVTRKCVLPYTOPSVSKEDYISLQPDRLSHLV-----VPLAQHVQPPPP 139
QY 105 FNVATYFSG-QYNTISWRSDEYDPAFYMLKKG-IQYELQYRNKGDPMVAVSPRRKLISVDSR 162
DB 140 KDISISPGDHFLLKMSVPLGDAQVSLSKQDIOFEVAAYKQLODSWB-----DAS 189
QY 163 S-----VSLPLEFRKDSSEYELQYRAGPMPGSGSYOGTSEMSWDPIYIQTOSSE 210
DB 190 SLHTCNLWVTLPEKLFIPNSITVARVRAQLAPGSSLSGRSGMSPEVHMSPTED 244

RESULT 2
A40091
Interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022
R:Itch, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara
Science 247, 324-327, 1990

A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
 A:Reference number: A40091; MUID:90117145
 A:Accession: A40091
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-878 <IT0>
 R:Gorman, D.M.
 submitted to GenBank, November 1989
 A:Reference number: A43022
 A:Accession: A43022
 A:Molecule type: mRNA
 A:Residues: 1-815, 'Q', 817-878 <GOR>
 A:Cross-references: GB:M29855; NID:9198342; PIDN:AAA9295.1; PID:9309406
 C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains 2 receptors.
 C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
 C:Keywords: cytokine receptor; duplication; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-878/Product: Interleukin-3 receptor beta chain #status predicted <MAT>
 F:23-440/Domain: extracellular #status predicted <EXT>
 F:39-236/Domain: cytokine receptor homology <CRS1>
 F:54-433/Domain: cytokine receptor homology <CRS2>
 F:41-462/Domain: transmembrane #status predicted <TM>
 F:463-878/Domain: intracellular #status predicted <INT>

Query Match 12.1%; Score 145; DB 1; Length 878;
 Best Local Similarity 23.0%; Pred. No. 8.3e-05;
 Matches 54; Conservative 30; Mismatches 91; Indels 60; Gaps 9;

QY 4 LVCTTYLTOTVCTLEMMNLHPSTLTLYWQD-----YEL-KDEATGCSL-- 48
 Db 37 LECYNDYTRNRIID-----SWADPEDAGLNMTLKLYHOLDKIQSVSCELSE 82
 QY 49 -----HRSANHATATYTCNM---DYFHEMADDFSVNITDQSGNYSQCGSFL 94
 Db 83 KLMMSCSPSSHRVCVPIYTRFNGNDYYSFQPDLDLQI-----MVP 130
 QY 95 LAESIRPAPPNTVTFSG-QYNISWRSDYEDPAFYMKGR-LQYELQYRNQDPMAVSP 152
 Db 131 LACHVPPPPKDIHISPSDHFLEWVSILGDSOVSWLSSKIDFEFVAYKRLQDSWEDA- 189
 QY 153 RRLKLVDSRSVSLPLFRKDSYELQVRAGPMGSSYQGTWSPSPVIRQ 207
 Db 190 --SSLTNSNQVNLKPLFNPSTIARVTRLSSGSSLSGRPSRWSPVHMDSQ 242

RESULT 3
 S68441
 A:Title: Leptin receptor, splice form Ob-Re - mouse
 A:Species: Mus musculus (house mouse)
 A:Update: 31-Dec-2000 #sequence, revision 31-Dec-2000 #text, change 31-Dec-2000
 C:Accession: S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fraz
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68441
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-805 <LEE>
 A:Cross-references: EMBL:U49110; NID:91195492; PIDN:AGC52424.1; PID:91195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439
 A:Gene: Ob-Re
 C:Keywords: alternative splicing; appetite

Query Match 12.1%; Score 144; DB 2; Length 805;
 Best Local Similarity 31.1%; Pred. No. 9.1e-05;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATSCSLHRSANHATATYTCMHDFH-----FMADDISVNTDQSGNYS 87
 Db 177 LKDSFQVQNCNLSRG-----ECHVPVPRAKLNTALLMYLEITSAGVSFQSPILMS 227
 QY 88 QEGCSFLIASIRPAPP--FNVTTFESGOYNISWRSDYEDPAFYMKGRLOVEYELQYRNNG 145
 Db 228 LQ--PMLV---VAPDPLGLHMEVTDGNLKSISWDSQYAPF-----PLQYQVATLENS 276
 QY 146 DPMVSPRRKLISVDSRSV-SLLPLFRKDSYELQVRAGPMGSSYQGTWSEWSDPVIF 204
 Db 277 T--IVRAAIEIVATSLVDVSLP-----GSSYEYGVRSKRLDGS---GVMSDMSPPQVF 326
 QY 205 QYQ 207
 Db 327 YTQ 329

RESULT 4
 S68439
 A:Title: Leptin receptor, splice form Ob-Rc - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-2000 #sequence, revision 31-Dec-2000 #text, change 31-Dec-2000
 C:Accession: S68439; S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68439
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 664-892 <LEE1>
 A:Cross-references: EMBL:U49108; NID:91195488; PIDN:AGC52422.1; PID:91195489
 A:Experimental source: splice form Rc; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Accession: S68441
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-796, GMCYVLPMD, <LEE2>
 A:Cross-references: EMBL:U49110; NID:91195492; PIDN:AGC52424.1; PID:91195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
 C:Genetics:
 A:Gene: Ob-Rc
 C:Keywords: alternative splicing; appetite

Query Match 12.1%; Score 144; DB 2; Length 892;
 Best Local Similarity 31.1%; Pred. No. 0.0001;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATSCSLHRSANHATATYTCMHDFH-----FMADDISVNTDQSGNYS 87
 Db 177 LKDSFQVQNCNLSRG-----ECHVPVPRAKLNTALLMYLEITSAGVSFQSPILMS 227
 QY 88 QEGCSFLIASIRPAPP--FNVTTFESGOYNISWRSDYEDPAFYMKGRLOVEYELQYRNNG 145
 Db 228 LQ--PMLV---VAPDPLGLHMEVTDGNLKSISWDSQYAPF-----PLQYQVATLENS 276
 QY 146 DPMVSPRRKLISVDSRSV-SLLPLFRKDSYELQVRAGPMGSSYQGTWSEWSDPVIF 204
 Db 277 T--IVRAAIEIVATSLVDVSLP-----GSSYEYGVRSKRLDGS---GVMSDMSPPQVF 326
 QY 205 QYQ 207
 Db 327 YTQ 329

RESULT 5
 S68437
 A:Title: Leptin receptor, splice form Ob-Ra - mouse

Query Match	12.1%	Score 144;	DB 2;	length 1162;
Best Local Similarity	31.1%	Pred. No. 0.00015;		
Best Local				
Matches	57;	Conservative	22;	Mismatches 60;
				Indels 44;
				Gaps 11;

[illegible]

RESULT 9
A35052
Interleukin-2 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 05-Nov-1999
C:Accession: A35052
R:Kono, T.; Doi, T.; Yamada, G.; Hatakeyama, M.; Minamoto, S.; Tsudo, M.; Miyasaka, M.;
Proc. Natl. Acad. Sci. U.S.A. 87, 1806-1810, 1990
A:Title: Murine interleukin 2 receptor beta chain: dysregulated gene expression in lymphoma
A:Reference number: A35052; MUID:90175385
Accession: A35052

Query Match	11.8%	Score 141.5	DB 2	Length 539
Best Local Similarity	22.5%	Pred. No. 9.1e-05		
Matches 54	Conservative 43	Mismatches 86	Indels 57	Gaps 12

QY	1	CPDLGVCYDYLDTQVTCILEEMWMLABSTJTLWMOQDYEBELKDEATSCSLRSXAHNTHAVY	60
Db	31	CSHLECFANSRANVSC-----MMS-HEEALNV-----TTCVHAQK-NIRHWK	72
QY	61	TCHMDVFH-----FMADIFSVNIT--DOSGNYSOEGCSFLLAESIK	100
Db	73	TCELLVWQASWACNMLIGSPESOSTLSVDLLDINNVACMEKGGMRVRYCTCFHFEDNIR	132
QY	101	PAPPENVTVTF--SCQYINISWR-----SYEDPAFVMLGKGLQYELQYRNGRDPMWVSPRR	154

```

Db 133 LVAPHSLOYLHIDTQRCNISMKNVSQVSHIYIP-----YLEFARRKLLGHSMEDA--- 182
QY 155 KLIYSDRSVSLPLPEFFKDSYELQVRAGMPSGSGYTMSEMSDPIVIFOTO-SEELKE 2133
    ::::: - - - ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 183 SVLSLAKGQGNLPLEMLIPSTSYEVQYRVKQGRNNT--GTMSPSPSGLFTFRTTRADPMKE 240

```

RESULT 10
B45266
MPL-k protein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence-revision 27-Jun-1994 #text-change 05-Nov-1999
C:Accession: B45266
R:ViSon, I.; Mornon, J.P.; Coccault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, P.; Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl proto-oncogene
A:Reference number: A45266; MUID:92302297
A:Accession: B45266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-579 <VIG>
A:Cross-references: GB:M90103; NID:g184262; PIDN:AAA69972.1; PID:g184263

	Query March	11.68:	Score 139:	DB 2:	Length 579:
	Best Local Similarity	24.0%:	Pred. No.	0.00017:	
	Matches 59:	Conservative 25:	Mismatches 76:	Indels 86:	Gaps
OY	4 LVCVTDYLQTYICILMNNLHPSTLTTLTWODQYELEDEATCSCL--HRSANNHTAHAY- 60	: :	: :	: :	
Dd	289 LCCEFLDLKNTYC-----QMQQO-----DHASQGFEYHSRARCPRDRYP 329	: :	: :	: :	
OY	61 -----TCHM-----DVHFPMADIFSVNITPQSGNYSEGCS-F 93	: :	: :	: :	
Dd	330 IWENCEEKEKNPGIQLPQFSRCFHKSNDISIHL-----VEYTARGTYSIYLGSF 363	: :	: :	: :	
OY	94 LLAESIK-PAPFPNVTVTFSSQYNISWSDVEDPAFYMLKGLOLEYOLYRNRG-DPWAVS 151	: : : : :	:	:	:
Dd	384 WIHGAVRPLPTNLHMREISSGHLELV---QHSSMAAO-ETCYOLRYRTGECHODKV- 437	: :	: :	: :	
OY	152 PRRKIIVDSNSVSLLP-----LEFRKDSSELVOVGAGPMGGSYCGGWSPWPVI 203	: :	: :	: :	
Dd	438 -----LEPLLARGGLTELRPSRKRLQGRRA RLNGPLPYQGPWSMSMDPTR 462	: :	: :	: :	

```

Oy      204  F0T0S0 209
        :| :|
Db      483  V0T0T0 488

RESULT  11
A45266
MPL-P protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A45266
R:Vison, I.; Mornon, J.P.; Coccault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht,
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl
A:Reference number: A45266; MUID:92302297
A:Accession: A45266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-635 <V16>
A:Cross-references: GB:M90102; NID:g184260; PIDN:AAA69971.1; PID:g184261
:Keywords: transmembrane protein

```

	Query Match	11.68;	Score 139,	DB 2:	length 635;
	Best Local Similarity	24.0%;	Pred. No.	0.00019;	
	Matches	59;	Conservative	25;	Mismatches 76; Indels 86; Gaps
Oy	4 LVCTDYDYLQTVICILEMMNHLHPTLTFLTWODQYEEELKDEATSCSL--HRSAHNHTATY-	60			


```

Db      289  LQCTFLDKNVTCT-----QWQDQ-----DHMSQGFPHSHARCCPRDRPT 329
QY      61  -----TCHM-----DVHFMAADIFSVNITDQSNYSQEGGS-F 93
Db      330  IWENCEEERKTNPLQTPQFSRCHFKFSRNDSIHIL-----VEYTTAPETVHSLGSPF 363
QY      94  LAESIK-PAPPFNWTVTFSGOVNISMRSYEDDPAPFYLKGLQYELQYVNRG-DEMAVS 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      384  WIHQAVALPPTPLNLMHRELSSCHLELEN-----QHPSSMAAO-ETCYQIURLTGBGHQDKV- 437
QY      152  PRKRLISVDSRSHSLP-----LEFRKDSYELQVRAAGPMGSSQYGTWSEWDPVYI 203
Db      438  -----LEPPLIARGGTLRLPRRSRYRLQRA-RINGPTRYQYPMSSWDPTK 482
QY      204  FQTOSE 209
Db      483  VEIATE 488

```

12
RESULT
142225

I:leptin receptor, isoform Ob-Rf - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
 C:Accession: S74225
 R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
 PERS Lett. 392, 87-90, 1996
 A:Title: A novel leptin receptor isoform in rat.
 A:Reference number: S74225; MUID:96368027
 A:Accession: S74225
 A:Molecule type: mRNA
 A:Residues: 1-895 <MAN>
 A:Cross-references: EMBL:U53144; NID:g1395212; PIDD:AA803088.1; PID:g1395213
 A:Experimental source: strain Sprague-Dawley, tissue type brain
 C:Genetics:
 A:Gene: rob-R
 C:Keywords: appetite; transmembrane protein
 I:840-860/Domain:transmembrane #status predicted <MAN>

Query Match	11.5%	Score 138	DB 2	Length 895
Best Local Similarity	30.9%	Pred. No. 0.00035		
Matches	36	Conservative	23	Mismatches 62; Indels 40; Gaps 11

QY	39	LKD--EATSCSLHRSAHNATHATYTCMDYFH-----FMADDIESVNTTDSGNYSC	89
	111 :	1 : 11 : 11 : 11 : 11 :	
	177	LKDSQFVQC-----NCSVRECECHVPBPRAKVANVALLIETTSAGVSFQSLMSLQ	229
	90	CGSFLLEASTPAPP--FNVTYVTSQGYNISMREDYEDPAPYMKGLQYELQYRRNGDP	147
		111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 :	
Db	230	--PMIV--VNPDPPLGLRMENVTDGNIKILSWDSQTAPF-----PLQYQVRKLENST-	277
	148	WAVSPRRKILSVDSRSV-SILPLEFRKDSYELQVRAGPMPGSSYQGTSMESDPVIFQI	206
		111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 :	
Db	278	-IVREAAEIVSDTSLVDSVLP-----GSSVEYGVRSKRIDGS--GVMSDWLSLPQLFTT	328
QY	207	Q 207	
Db	329	Q 329	

RESULT 13

leptin receptor Ob-Rb - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequenceRevision 13-Mar-1997 #textChange 01-Dec-2000
C:Accession: J04895, J04896, J04897, PC0184, J04797
R:Author: K. Ogawa, Y. Isse, N. Okazaki, T. Satoh, N. Masuzaki, H. Mori, K. Tamura
Biochem. Biophys. Res. Commun. 225, 75-83, 1996
A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-Identification
A:Reference number: J04895, M01D:960332408
A:Accession: J04895
A:Status: Preliminary

A:Molecule type: mRNA
A:Residues: 1-1162 <TAK>
A:Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAAI2831.1; PID:d1013515; PID:g15
A:Accession: J04896
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <TA2>
A:Cross-references: DDBJ:D85557
A:Accession: J04897
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796, 'G', '1157-1158, 'TWLIN' <TA3>
A:Cross-references: DDBJ:D85559
A:Rida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwayama, M.; Shima, K.
Biochem. Biophys. Res. Commun. 224: 597-604, 1996
A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
A:Reference number: P04184; MUID:96295531

Query Match	11.5%;	Score 138;	DB 2;	Length 1162;
Best Local Similarity	30.9%;	Pred. No. 0.0005;		
Matches 56;	Conservative 23;	Mismatches 62;	Indels 40;	Gaps 11;

QY	39	LKD--EATSCSLHRSAHNATATYCHMDVFN-----FMADDFSVNITDQSGNTSOE	89
	IKDSFQVQC-----NCSVRECECHVPYRAKVNTALLMYLEITSAGVSPQLMSLQ	229	
Db	177		
QY	90	CGSLIAESLKRAPP--FNVIYFSGGVYNTSMRSDVEDPAFVWKGKQLQYELQYRNNQDP	147
Db	230	--PKLV--VKPDPPLGLMVEYTDGNLKLKTSWDSQTAAP-----PLQYQVKTLENST-	277
QY	148	WAVSPRRKLIVSDSRGV-SLLPLERKDSXYELOVRAGPVGSSYQGTWSEMSDPLVIFQT	206
Db	278	IYREAEAIIVSDTSLIVDSVLP-----GSSYEVQYRKRKIDGS--GWSDPMSLPQLFTT	328
QY	207	Q	207
Db	329	Q	329

RESULT 14

Ae0386
 interleukin-4 receptor precursor - human
 N:Alternate names: IL-4 receptor
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C:Accession: Ae0386; A47603
 R:Galizzi, J.P.; Zuber, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kastelein, R.; Birtt Immunol. 2: 669-675, 1990
 A:Title: Molecular cloning of a cDNA encoding the human interleukin 4 receptor.
 A:Reference numbers: Ae0386; MUID:91120547
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 110.69 Seconds

(without alignments)
232.804 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTWILTPNGNEDTADFL.....QHWSEWSHPHMGSNSTSKEN 232

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues 747574

tal number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_032802:*

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- 2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
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- 7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
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- 11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
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- 18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1288	100.0	347	15	AA847149
2	1288	100.0	369	15	AA847148
3	1288	100.0	691	21	AAV92202
4	1288	100.0	694	21	AAV92201
5	1288	100.0	694	21	AAV92203
6	1282	99.5	482	15	AAW31646
7	1277	99.1	230	15	AA847151
8	1277	99.1	252	15	AA847150
9	1272	98.8	230	16	AA829934
10	960	74.5	363	22	AA871682
11	854.5	66.3	369	15	AA859094

12	542	42.1	121	21	AA600283	Human secreted pro
13	215	16.7	561	22	AA69138	Canine IL-13Ralpha
14	215	16.7	561	22	AA69141	Canine IL-13Ralpha
15	215	16.7	563	22	AA69140	Canine IL-13Ralpha
16	215	16.7	565	22	AA69139	Canine IL-13Ralpha
17	213	16.5	318	22	AA69137	Canine IL-13R extr
18	213	16.5	365	22	AA69136	Canine interleukin
19	213	16.5	386	22	AA69135	Canine interleukin
20	207	16.1	315	19	AA856261	Mature interleukin
21	207	16.1	339	19	AA856260	Construct containi
22	207	16.1	380	18	AAW24972	Human interleukin-
23	207	16.1	380	18	AAW35295	Human IL-13 bindin
24	207	16.1	380	18	AAW36613	Human Zcytor2 cyto
25	207	16.1	380	19	AAW41520	Human HR-1 recepto
26	207	16.1	380	19	AAW41502	Human cytokine/pep
27	207	16.1	380	19	AAW33603	Homo sapiens HR-1
28	207	16.1	380	21	AAV95296	IL-13 binding chai
29	207	16.1	380	22	AAV95296	Amino acid sequenc
30	207	16.1	380	22	AAV95296	Human interleukin
31	207	16.1	380	22	AAV95296	Human IL-13 recept
32	206	16.0	255	22	AA69134	Canine interleukin
33	203	15.8	380	18	AAW36614	Human Zcytor2 cyto
34	199.5	15.5	383	18	AAW35294	Murine IL-13 bindi
35	199.5	15.5	383	21	AAV95295	IL-13 binding chai
36	199.5	15.5	383	22	AAV95295	Murine interleukin
37	199.5	15.5	383	22	AAV95295	Mouse IL-13 recept
38	183.5	14.2	372	18	AAW36616	Celebus macaque Zc
39	180	14.0	426	18	AAW09821	Mouse interleukin-
40	178	13.8	426	18	AAW09822	Human interleukin-
41	178	13.8	427	18	AAW24973	Human interleukin-
42	178	13.8	427	22	AAW19807	Human interleukin-
43	178	13.8	784	21	AAV92207	Human interleukin-
44	178	13.8	793	21	AAV92208	IL-13/IL-4 dual tr
45	178	13.8	793	21	AAV92208	IL-13/IL-4 dual tr

ALIGNMENTS

RESULT 1

AA847149

ID AA847149 standard; Protein: 347 AA.

XX

AC AA847149;

XX

DT 13-JUN-1994 (first entry)

XX

DE IL-2 receptor gamma chain.

XX

XX Interleukin-2 receptor gamma chain; IL-2; receptor; Immunoregulator;

KW rheumatoid arthritis; transplant rejection; primer;

KM polymerase chain reaction; PCR; amplification.

XX

OS Homo sapiens.

XX

PN EP578932-A.

XX

PD 19-JAN-1994.

XX

PF 22-APR-1993; 93EP-0106561.

XX

PR 23-APR-1992; 92JP-0104947.

XX

PA (AJIN) AJINOMOTO KK.

PA (SUGA) SUGAMURA K.

XX

PI Aaso H, Hamuro J, Nakamura M, Shimamura T, Sugamura K;

PI Suzuki M, Takeshita T;

XX

DR WPI; 1994-017546/03.

DR N-PSDB; AA054829.

XX

PT DNA and protein sequences of IL-2 gamma chain - useful as immune

PT regulatory agents for treatment of e.g. rheumatoid arthritis and
PT transplant rejection

XX Claim 4; Page 41; 50pp; English.

CC The human IL-2 receptor gamma chain preform (AA47148), including the
CC signal peptide, is encoded by the sequence given in AA054828. The
CC mature protein (AA47149) is encoded by sequence AA054829. A soluble
CC form of IL-2 receptor gamma chain (AA47150) is encoded by AA054830,
CC while a soluble form suitable for expression in prokaryotes (AA47151)
CC is encoded by AA054831. Primers 1-6 (AA054820-25) are based on the N-
CC terminal sequence of IL-2 receptor gamma chain, and are used to
CC isolate IL2 receptor gamma chain receptor cDNA. Primers AA054826-27
CC are used to obtain the protein given in AA47151.

XX Sequence 347 AA;

Query Match 100.0%; Score 1288; DB 15; Length 347;

Best Local Similarity 100.0%; Pred. No. 6, 7e-116; Mismatches 0; Gaps 0;

Matches 232; Conservative 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTADFLTTPDLSYSTLPPEVQCFVFNVEYMNCTWNSSEPPQ 60

DB 1 Intlltpngnedtadflttmptdlsysvstlplpevcfivfnveymctwnssseppq 60

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCQLOKKEIHLVQYRTDWSMTESQV 120

DB 61 tnltlhwynksndndkvkcsnylfseetsgcqlqkkeihlyqfvtvqldqpreprq 120

QY 121 TQMLKIQNLVTPAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDWSMTESQV 180

DB 121 tqmlkignltvlpapenltlkhlsesqlelnwnrflnhclehlvqyrtcdwshwteqsv 180

QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHMSEMSHPIMGSNTSKEN 232

DB 181 dyrhkftslpsvdgqkrytfrvrsrfrnplcgsaqhmseshpilhwsntsksn 232

RESULT 2

AA47148

ID AA47148 standard; Protein: 369 AA.

AC AA47148;

DT 13-JUN-1994 (first entry)

XX IL-2 receptor gamma chain.

DE Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;

KM Rheumatoid arthritis; transplant rejection; primer: PCR;

KW polymerase chain reaction; amplification; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..22

FT /label= Sig_peptide

PN EP578932-A.

PD 19-JAN-1994.

PF 22-APR-1993; 93EP-0106561.

PR 23-APR-1992; 92JP-0104947.

XX (AJIN) AJINOMOTO KK.

PA (SUGA) SUGAMURA K.

XX Asao H, Hamuro J, Nakamura M, Shimamura T, Sugamura K;

PI Suzuki M, Takeshita T;

XX

DR WPI: 1994-017546/03.

DR N-PSDB; AA054828.

XX DNA and protein sequences of IL-2 gamma chain - useful as immune

PT regulatory agents for treatment of e.g. rheumatoid arthritis and

PT transplant rejection

XX Disclosure: Page 16-17, 29-30; 50pp; English.

XX The human IL-2 receptor gamma chain preform (AA47148), including the
XX signal peptide, is encoded by the sequence given in AA054828. The
XX mature protein (AA47149) is encoded by sequence AA054829. A soluble
XX form of IL-2 receptor gamma chain (AA47150) is encoded by AA054830,
XX while a soluble form suitable for expression in prokaryotes (AA47151)
XX is encoded by AA054831. Primers 1-6 (AA054820-25) are based on the N-
XX terminal sequence of IL-2 receptor gamma chain, and are used to
XX isolate IL2 receptor gamma chain receptor cDNA. Primers AA054826-27
XX are used to obtain the protein given in AA47151.

XX Sequence 369 AA;

Query Match 100.0%; Score 1288; DB 15; Length 369;

Best Local Similarity 100.0%; Pred. No. 7, 3e-116; Mismatches 0; Indels 0; Gaps 0;

Matches 232; Conservative 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTADFLTTPDLSYSTLPPEVQCFVFNVEYMNCTWNSSEPPQ 60

DB 23 Intlltpngnedtadflttmptdlsysvstlplpevcfivfnveymctwnssseppq 82

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCQLOKKEIHLVQYRTDWSMTESQV 120

DB 83 tnltlhwynksndndkvkcsnylfseetsgcqlqkkeihlyqfvtvqldqpreprq 142

QY 121 TQMLKIQNLVTPAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDWSMTESQV 180

DB 143 tqmlkignltvlpapenltlkhlsesqlelnwnrflnhclehlvqyrtcdwshwteqsv 202

QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHMSEMSHPIMGSNTSKEN 232

DB 203 dyrhkftslpsvdgqkrytfrvrsrfrnplcgsaqhmseshpilhwsntsksn 254

RESULT 3

AA47202

ID AA47202 standard; Protein: 691 AA.

AC AA47202;

DT 01-AUG-2000 (first entry)

XX Fusion polypeptide 603, IL-4 trap.

DE Fusion polypeptide 603, IL-4 trap.

KM IL-4 trap; cytokine; antagonist; CNTF; receptor; fusion protein;

KW cytotactic; immunomodulator; osteopathic.

OS Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..22

FT /label= Sig_peptide

PN WO200018932-A2.

PD 06-APR-2000.

PF 22-SEP-1999; 99WO-US22045.

PR 25-SEP-1998; 98US-0101858.

XX 19-MAY-1999; 99US-0313942.

PA (REGF-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

PI WPI; 2000-293165/25.

XX

DR N-PSDB; AAA09044.

XX Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
to form a nonfunctional complex

XX Example 6; Fig 22A-D; 152pp; English.

CC This sequence shows fusion polypeptide 603, which is capable of
CC binding cytokine IL-4 to form a non-functional complex.
CC The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to
CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization, the
CC soluble alpha specificity determining component of the receptor
CC (SR-alpha) and the extracellular domain of the first beta signal
CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (ciliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the presence of a ligand, a non-functional intermediate complex, the
CC consisting of the ligand, its alpha receptor and its beta-1 receptor
CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.
CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.

XX Sequence 691 AA;

S0 Query Match 100.0%; Score 1288; DB 21; Length 691;

Best Local Similarity 100.0%; Pred. No. 1.8e-115; Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTADFLITPTDLSVSTLPLPEVOCFVNEVMNCTMNSSEPP 60
DB |||||||
DB 23 Inttiltpngnedtadflitpmtslsvstlplpevgcfvnevmnctwnsseppq 82
QY 61 TNLTLHWYKNSDNDKVKQKSHYLFSEETISGCOLQKKEHLVQTFVYVQLODRPRRQA 120
DB |||||||
DB 83 TNLTLHWYKNSDNDKVKQKSHYLFSEETISGCOLQKKEHLVQTFVYVQLODRPRRQA 142
QY 121 TQMLKQLONLVIWAPENLTLHKLSQSLELMNMRFLNHCLEHLVQYRTDMDHSWTQSGV 180
DB |||||||
DB 143 TQMLKQLONLVIWAPENLTLHKLSQSLELMNMRFLNHCLEHLVQYRTDMDHSWTQSGV 202
QY 181 DYRHKFSLPSVDGQKRYTFVRVSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB |||||||
DB 203 DYRHKFSLPSVDGQKRYTFVRVSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 4
AA92201
ID AA92201 standard; protein; 694 AA.

XX AA92201;

XX 01-AUG-2000 (first entry)

XX Fusion polypeptide 424, IL-4 trap.

XX IL-4 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
KM Cytostatic; Immunomodulator; osteopatinic.
XX

OS Synthetic.

OS Homo sapiens.

PN WO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99WO-US22045.

XX 25-SEP-1998; 98US-0101858.

XX 19-MAY-1999; 99US-0313942.

XX (REGG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

DR WPI: 2000-293165/25.

XX N-PSDB; AAA09043.

PT Isolated nucleic acid molecule for treating cytokine-related diseases
or disorders encodes a fusion polypeptide capable of binding a cytokine
to form a nonfunctional complex

XX Example 6; Fig 21; 152pp; English.

CC This sequence shows fusion polypeptide 424, which is capable of
CC binding cytokine IL-4 to form a non-functional complex.
CC The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to
CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization, the
CC soluble alpha specificity determining component of the receptor
CC (SR-alpha) and the extracellular domain of the first beta signal
CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (ciliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the presence of a ligand, a non-functional intermediate complex,
CC consisting of the ligand, its alpha receptor and its beta-1 receptor
CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.
CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.

S0 Sequence 694 AA;

Query Match 100.0%; Score 1288; DB 21; Length 694;

Best Local Similarity 100.0%; Pred. No. 1.8e-115; Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTADFLITPTDLSVSTLPLPEVOCFVNEVMNCTMNSSEPP 60
DB |||||||
DB 23 Inttiltpngnedtadflitpmtslsvstlplpevgcfvnevmnctwnsseppq 82
QY 61 TNLTLHWYKNSDNDKVKQKSHYLFSEETISGCOLQKKEHLVQTFVYVQLODRPRRQA 120
DB |||||||
DB 83 TNLTLHWYKNSDNDKVKQKSHYLFSEETISGCOLQKKEHLVQTFVYVQLODRPRRQA 142
QY 121 TQMLKQLONLVIWAPENLTLHKLSQSLELMNMRFLNHCLEHLVQYRTDMDHSWTQSGV 180
DB |||||||
DB 143 TQMLKQLONLVIWAPENLTLHKLSQSLELMNMRFLNHCLEHLVQYRTDMDHSWTQSGV 202
QY 181 DYRHKFSLPSVDGQKRYTFVRVSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232

|||||
 Db 203 dyrhkfslpsvqgkrytlrvsrfrnplcgsgqhwsewshpnhgnsntskn 254

RESULT 5
 ID AAY92203 standard; Protein: 694 AA.
 XX AAY92203;
 AC AAY92203;
 XX 01-AUG-2000 (first entry)
 DT
 DE fusion polypeptide 622, IL-4 trap.
 XX
 XX IL-4 trap; cytokine; antagonist; CNTP; receptor; fusion protein;
 KM cytostatic; immunomodulator; osteopathic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 OS WO200018932-A2.

PD 06-APR-2000.
 XX 22-SEP-1999; 99WO-US22045.
 PF
 XX 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REGG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI: 2000-293165/25.
 DR N-PSDB; AAA9045.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 XX Example 6; Fig 23A-D; 152pp; English.

CC This sequence shows fusion polypeptide 622, which is capable of
 CC binding cytokine IL-4 to form a non-functional complex.
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTP (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTP consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

Sequence 694 AA;

Query Match 100.0%; Score 1288; DB 21; Length 694;
 Best Local Similarity 100.0%; Pred. No. 1,86-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTADFTLTPTDLSVSTLPPEVOCEVFNVEYKNCWNSSEPPQ 60
 DB 23 Intlltpngnedtadftltptdlsvstlpipevcvfnveymctwnssseppq 82
 QY 61 TNLTLHWYKNSDNDKQKCSHYLFSEETSGGCOLKKEITHLYGFVVOLODPPRPAOA 120
 DB 83 tnltlhwynsdndkqkcschylfseetsggcolkkeithlygfvvooldpprpa 142
 QY 121 TQMLKIQMLVPMAPENLTLHKLSQDLIMNNRFLNHCLEHLVQYRTDMDHSWTQSV 180
 DB 143 tqmlkqlmlypwapenlthklsesqlelmnnrflnhclehlyqyrtcdhswtqsv 202
 QY 181 DYRHKFSLPSVDGOKRYTFVRSRFNPDLGSAOHMSEMSHPIMWSNFSKEN 232
 DB 203 dyrhkfslpsvqgkrytlrvsrfrnplcgsgqhwsewshpnhgnsntskn 254

RESULT 6
 ID AAW31646 standard; Protein: 482 AA.
 XX AAW31646;
 AC AAW31646;
 XX 21-MAY-1998 (first entry)
 DT
 XX
 DE Human cytokine receptor gc chain-ig fusion protein.
 XX
 XX Cytokine receptor; gamma common chain; gc chain; human;
 KW blocking agent; monoclonal antibody; CP.B8; immunological disease;
 KW myasthenia gravis; rheumatoid arthritis; lupus; multiple sclerosis;
 KW insulin-dependent diabetes; inflammatory bowel disease;
 KW sympathetic ophthalmia; uveitis; allergy; asthma; infection;
 KW graft versus host disease; psoriasis; immunosuppressive; therapy.
 XX
 OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers
 FH Protein 1..254
 FT /note="gc chain N-terminal region"
 FT 255..482
 FT /note="IgG1 constant region"
 FT 255..264
 FT /note="IgG1 hinge region"
 FT 264..482
 FT /note="IgG1 CH2 and CH3 constant domains1"

XX W09743416-A1.
 XX 20-NOV-1997.
 PD
 XX 09-MAY-1997; 97WO-US07870.
 PF
 XX 10-MAY-1996; 96US-0017466.
 PR
 XX (BIOJ) BIOGEN INC.

XX Benjamin CD, Burkly LC, Hession C, Whitty A;
 PI
 XX WPI: 1998-008885/01.
 DR N-PSDB; AAT97439.

PT Blocking agents of the gamma common chain of cytokine receptors -
 PT particularly monoclonal antibodies, used to induce T cell anergy for
 PT treatment of immunological diseases

PS Example 1; Page 79-80; 11pp; English.

CC This polypeptide comprises a fusion between the N-terminal 254
 CC amino acids of the human mature cytokine receptor gamma common (gc)

CC chain ad the hinge region and CH2 and CH3 constant domains of
CC human IgG1. The fusion was expressed from clone pLB001 (see
CC AA9747439) in COS-7 cells, and used to generate murine anti-human gC
CC specific monoclonal antibodies (MAbs), including CP.B8 produced by
CC hybridoma ATCC HB 12107. The invention provides compositions and
CC methods for inhibiting cytokine signalling using gC chain blocking
CC agents for the treatment of immunological diseases such as
CC myasthenia gravis, rheumatoid arthritis, lupus, multiple sclerosis,
CC insulin-dependent diabetes, inflammatory bowel disease, sympathetid
CC ophthalmia, uveitis, allergy, asthma, parasitic infection, graft
CC vs. host disease or psoriasis. A preferred gC blocking agent is
CC Mab CP.B8 or its Fab fragment (see also AA931047-48).

sq Sequence 482 AA;

Query Match	99.58;	Score 1282;	DB 19;	Length 482;
Best Local Similarity	99.68;	Pred. No. 4e-115;		
Matches 231; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	LNTLTTPGKNDTADDFLTPTDLSLSTPLREYCCFFANVYKNCWMSNSSEPOP	60
Db	23	Intltltprgnedtaafitltprtdlsstlrlpveqcvfivveymctmsseppr	82
Qy	61	TNLTTHWYKNSNDKRYKCSHYLFSEELTSGCOLKKEIHLVQTFVYLODPREPRROA	120
Db	83	tnltthwyknsndkvqckeshylfseelstsgqldkkehlygtfvqldqpreprg	142
Qy	121	TQWIKIÖNLVTPWAPENLTTLKLSSEOLNMMNREFLNHCENLVQYRTDMDHSWTEQSV	180
Db	143	tqmklqgrnlvtpwapeenlttlklsesqldetlmmnrflmnclehlvqyrtddhswteqsv	202
Qy	181	DYHNKRSLPSYDQGRYRYEFRVRSRFPNLGSAOHSEWSEHPRIMWSNNSTSKN	232
Db	203	drynksrslpsvdqgrkrymfrvtrstfmlpdsasqmwsewhprlmwsnstskn	254

RESULT 7

ID AAR47151 standard; protein; 230 AA.

AC AAR47151;

DT 13-JUN-1994 (first entry)

DE IL-2 receptor gamma chain.

Interleukin-2 receptor gamma chain; IL-2; receptor; rheumatoid arthritis; transplant rejection; primer; polymerase chain reaction; PCR; amplification.

05 Homo sapiens.

PN EP578932-A.

PD 19-JAN-1994

PF 22-APR-1993; 93EP-0106561.

PR 23-APR-1992; 92JP-0104947.

PA (AJIN) AJINOMOTO KK
PA (SUGA/) SUGAMURA K.

PI Asao H, Hamuro J, Nakamura M, Shimamura T, Sugamura K,
PI Suzuki M, Takeshita T;

DR WPI; 1994-017546/03.
DR N-PSDB; AAQ54831.

PT DNA and protein sequences of IL-2 gamma chain - useful as immune
PT regulatory agents for treatment of e.g. rheumatoid arthritis and
PT transplant rejection

XX Disclosure; Page 22-23, 35-36; 50pp; English
PS

CC The human IL-2 receptor gamma chain preform AAR471149), including the
CC signal peptide, is encoded by the sequence given in A05048288. The
CC mature protein (AAR77149) is encoded by sequence A0504829. A soluble
CC form of IL-2 receptor gamma chain (AAR47150) is encoded by A0504830.
CC while a soluble form suitable for expression in prokaryotes (AAR77151
CC is encoded by A0504831. Primers 1-6 (A0504820-25) are based on the N
CC terminal sequence of IL-2 receptor gamma chain, and are used to
CC isolate IL2 receptor gamma chain receptor cDNA. Primers A0504826-27
CC are used to obtain the protein given in AAR77151.

SQ Sequence 230 AA:

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Query Match      99.1%;   Score 1277;   DB 15;   Length 230;
Best Local Similarity -100.0%;   Pred. No. 4.4e-115;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 INTTITFPGNEDTADPELITFMTPLDLSIYSTPLPEVOCAFNEVNYXNACWNSSEPOF 60
Db 1 INTTITFPGNEDTADPELITFMTPLDLSIYSTPLPEVOCFIVFVNYXNACWNSSEPOF 60
OY 1 INTTITFPGNEDTADPELITFMTPLDLSIYSTPLPEVOCFIVFVNYXNACWNSSEPOF 60
Db 1 INTTITFPGNEDTADPELITFMTPLDLSIYSTPLPEVOCFIVFVNYXNACWNSSEPOF 60
OY 61 TNLTEHYWYKNSDNDKRVKCSHYLFSEETISGCOLKKEIHLVQTFVVOLODPREPRQA 120
Db 61 TNLTEHYWYKNSDNDKRVKCSHYLFSEETISGCOLKKEIHLVQTFVVOLODPREPRQA 120
OY 61 TNLTEHYWYKNSDNDKRVKCSHYLFSEETISGCOLKKEIHLVQTFVVOLODPREPRQA 120
Db 61 TNLTEHYWYKNSDNDKRVKCSHYLFSEETISGCOLKKEIHLVQTFVVOLODPREPRQA 120
OY 121 TQWLKTLQNLVITWAPEDNLTLEKLSSESOLELNNNNRFLNNCLNHLVQYRTDMDHSWTQSY 180
Db 121 TQWLKTLQNLVITWAPEDNLTLEKLSSESOLELNNNNRFLNNCLNHLVQYRTDMDHSWTQSY 180
OY 121 TQWLKTLQNLVITWAPEDNLTLEKLSSESOLELNNNNRFLNNCLNHLVQYRTDMDHSWTQSY 180
Db 121 TQWLKTLQNLVITWAPEDNLTLEKLSSESOLELNNNNRFLNNCLNHLVQYRTDMDHSWTQSY 180
OY 181 DYHHRKSLPSVDGOKRYRFRVRKSRFNLQCSAQHWSBWSPIIHMKSNSNISK 230
Db 181 DYHHRKSLPSVDGOKRYRFRVRKSRFNLQCSAQHWSBWSPIIHMKSNSNISK 230
OY 181 DYHHRKSLPSVDGOKRYRFRVRKSRFNLQCSAQHWSBWSPIIHMKSNSNISK 230
Db 181 DYHHRKSLPSVDGOKRYRFRVRKSRFNLQCSAQHWSBWSPIIHMKSNSNISK 230

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RESULT

ID AAR47150 standard; Protein; 252 AA

AC AAR47150;

DT 13-JUN-1994 (first entry)

DE IL-2 receptor gamma chain.

KW Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator
KW rheumatoid arthritis; transplant rejection; primer;
KW polymerase chain reaction; PCR; amplification; ss.

05 Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
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93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT /label= Sig_peptide

PN EP578932-A.

PD 19-JAN-1994

PF 22-APR-1993; 93EP-0106561.

PR 23-APR-1992; 92JP-0104947.

XX
PA
(AJIN) AJINOMOTO KK.
AJINOMOTO K.

XX Asao H, Hamuro J,
PI

```
XX DNA and protein sequences of IL-2 gamma chain - useful as immune
PT regulatory agents for treatment of e.g. rheumatoid arthritis and
PT transplant rejection
XX
XX Disclosure; Page 21-22, 34-35; 50pp; English.
XX
CC The human IL-2 receptor gamma chain preform (AAR47148), including the
CC signal peptide, is encoded by the sequence given in AA054828. The
CC mature protein (AAR47149) is encoded by sequence AA054829. A soluble
CC form of IL-2 receptor gamma chain (AAR47150) is encoded by AA054830.
CC while a soluble form suitable for expression in prokaryotes (AAR47151)
CC is encoded by AA054831. Primers 1-6 (AA054820-25) are based on the N-
CC terminal sequence of IL-2 receptor gamma chain, and are used to
CC isolate IL2 receptor gamma chain receptor cDNA. Primers AA054826-27
CC are used to obtain the protein given in AAR47151.
XX
SQ Sequence 252 AA:
Query Match 99.1%; Score 1277; DB 15; Length 252;
Best Local Similarity 100.0%; Pred. No. 4,9e-115;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LNTTILTPNGNEEDTADFLITMPDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
DB 23 Lnttliltpngnedtadflitmpdlsvstlplpevqcfvfnveymctwnsssepp 82
OY 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCOLQKKEIHLVQTFVYQLODPPRPRQA 120
DB 83 tnltlhwknsdndkvqcskshylfseetsgcqlkkeihlyqtfvvyqldpprprqa 142
OY 121 TQMLKQLNLYIPAPENLTLHKLSQSLELNMNRFNLNHCLEHLVQYRTDMDHSWTQSV 180
DB 143 tqmlkqlnlyipapenltlhklsesqlelnmnrfnlnclehlvqyrtddhswtqsv 202
OY 181 DYRKFSLSVSDGKRYTFVRNRFNPLCGSAQHSEWSHPIMGSSNTS 230
DB 203 dyrkfslspvdgkrytfvrnsrtnplcgasqhwsewsbplhwgsntsk 252
RESULT 9
AAR82934
ID AAR82934 standard; Protein; 230 AA.
XX
AC AAR82934;
XX
XX 26-FEB-1996 (first entry)
XX
XX Interleukin 4 component common to the IL-2 receptor gamma chain.
XX
XX Interleukin-4; IL-4; gamma chain component; immunosuppressants;
XX anti-allergy agent; signal transmsion inhibitor; autoimmune;
XX disease; anti-inflammatory; anaphylactic shock; bronchial asthma;
XX Interleukin-2; IL-2; atopic dermatitis; urticaria.
XX
XX Homo sapiens.
XX
XX JF07149662-A.
XX
XX 13-JUN-1995.
XX
XX PD 07-SEP-1994; 94JP-0213706.
XX
XX PF 08-SEP-1993; 93JP-0223574.
XX
XX PR (AJIN) AJINOMOTO KK.
XX (SUGA/) SUGAMURA K.
XX
XX WPI; 1995-243601/32.
XX
XX DR N-PSDB; AAT04952.
XX
XX Novel interleukin-4 receptor monoclonal antibodies inhibit signal
```

```
PT transmission - useful as immunosuppressants and anti-allergy agents.
XX
XX Example 1; Page 9; 11pp; Japanese.
XX
XX AAT04952 encodes AAR82934 a component of the IL-4 receptor common to
XX the IL-2 receptor gamma chain molecule, which was used to generate
XX anti-IL-4 receptor monoclonal antibodies (mabs). The mabs (IL-4
XX signal transmission inhibitors) can be used as immunosuppressants
XX and anti-allergy agents, for the treatment of autoimmune and chronic
XX inflammatory diseases, e.g. anaphylactic shock, bronchial asthma,
XX atopic dermatitis and urticaria.
XX
XX
SQ Sequence 230 AA:
Query Match 98.8%; Score 1272; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 1,3e-114;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LNTTILTPNGNEEDTADFLITMPDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
DB 2 Lnttliltpngnedtadflitmpdlsvstlplpevqcfvfnveymctwnsssepp 61
OY 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCOLQKKEIHLVQTFVYQLODPPRPRQA 120
DB 62 tnltlhwknsdndkvqcskshylfseetsgcqlkkeihlyqtfvvyqldpprprqa 121
OY 121 TQMLKQLNLYIPAPENLTLHKLSQSLELNMNRFNLNHCLEHLVQYRTDMDHSWTQSV 180
DB 122 tqmlkqlnlyipapenltlhklsesqlelnmnrfnlnclehlvqyrtddhswtqsv 181
OY 181 DYRKFSLSVSDGKRYTFVRNRFNPLCGSAQHSEWSHPIMGSSNTS 229
DB 182 dyrkfslspvdgkrytfvrnsrtnplcgasqhwsewsbplhwgsntsk 230
RESULT 10
AAB71682
ID AAB71682 standard; protein; 363 AA.
XX
XX AAB71682;
XX
XX 10-MAY-2001 (first entry)
XX
XX Bos taurus interleukin-2 receptor gamma.
XX
XX
XX Cytokine receptor common gamma chain like; CRGCGU; human;
XX tumours; infections; inflammatory; immune disorder;
XX neurodegenerative; cardiovascular; disorder.
XX
XX Bos taurus.
XX
XX WO200112672-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22493.
XX
XX 18-AUG-1999; 99US-0376430.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SA, Rosen CA, Moore PA;
XX
XX WPI; 2001-147547/15.
XX
XX New nucleic acid molecule encoding a human cytokine receptor common
XX gamma chain like polypeptide, useful for treating, preventing and/or
XX diagnosing e.g. tumors, inflammatory diseases and immunodeficiency
XX conditions -
XX
XX Disclosure; Fig 2; 288pp; English.
XX
```


XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PS
 XX Claim 13; SEQ ID 4364; 71pp + CD-ROM; English.

CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.

Sequence 121 AA;

Query Match 42.1%; Score 542; DB 21; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.5e-44;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNTTITLPGNEDTADFLTTMPTDLSVSTLPLEVOCFVFNVEYMNCTWNSSEPPQ 60
 Db 23 LNTTITLPGNEDTADFLTTMPTDLSVSTLPLEVOCFVFNVEYMNCTWNSSEPPQ 82

OY 61 TNLTLHWYKNSDNDKVKOKCSHYLFSEETITSGCOLQKKE 99
 Db 83 tnltlhwynksndndkvkocshylfseeltsgcolqkke 121

RESULT 13
 AAU69138
 ID AAU69138 standard; Protein: 561 AA.
 AC AAU69138;
 XX
 XX 29-JAN-2002 (first entry)
 DE
 XX Canine IL-13Ralpha2/IgG-Fc fusion protein pCaIL-13Ralpha2-Fc-3523 561.
 DE
 XX Dog: interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
 immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
 immune response.
 KW
 XX Canis familiaris.
 OS
 XX WO200177332-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 09-APR-2001; 2001WO-US11498.
 PF
 XX 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 XX (HESK-) HESKA CORP.
 PA
 XX McCall CA, Tang L;
 PI
 XX WPI, 2001-657172/75.
 DR
 XX N-PSDB; AAS59970.
 DR
 XX Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -

XX Claim 46; Page 191-193; 221pp; English.

PS The invention concerns an isolated canine protein, preferably canine
 XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13 proteins
 CC and methods of isolating regulators in a canine. The regulators are useful
 CC for regulating an immune response in a canine. The regulators useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence represents a protein of the invention.

Sequence 561 AA;

Query Match 16.7%; Score 215; DB 22; Length 561;
 Best Local Similarity 26.1%; Pred. No. 4.7e-12;
 Matches 63; Conservative 37; Mismatches 103; Indels 38; Gaps 9;

OY 3 TTTITLPGNEDTADFLTTMPTDLSVSTLPLEVOCFVFNVEYMNCTWNSSEPPQ-P 60
 Db 105 tlytspggnret-----kqndcyyymkqylvcswkpgmgyhtd 145

OY 61 TNLTLHWYKNSDNDKVKOKCSHYLFSEETITSGCOLQKKEILVOTFYVQLDPPRE--PRR 118
 Db 146 tnytlfwyegldhs--aecdtyikvngkmgrcfylessdykdfyicvngsseqprr 203

OY 119 QATQMLKQNIIVYAPENLTILHKTSESQLELMNN--NFIWHCEHLVQYETDMDHSM 175
 Db 204 psytlfqlgqlqmpoylsitvknsseilnkwmmpkxpipakcflyelefed-qltw 262

OY 176 TEGSDVYRHKFSLPSVDGQKRYRFRVRSRFPNPLGSAQHSEMSHPILHW-----GSN 227
 Db 263 vtlvemeiqtlrtsnesqk-lcflvrskvnylsdsgdgiwsewdeqcgkdiwketgtn 321

OY 228 T 228
 Db 322 t 322

RESULT 14
 AAU69141
 ID AAU69141 standard; Protein: 561 AA.
 AC AAU69141;
 XX
 XX 29-JAN-2002 (first entry)
 DE
 XX Canine IL-13Ralpha2/IgG-Fc fusion protein pCaIL-13Ralpha2-Fc-B9 561.
 DE
 XX Dog: interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
 immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
 immune response.
 KW
 XX Canis familiaris.
 OS
 XX WO200177332-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 09-APR-2001; 2001WO-US11498.
 PF
 XX 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 XX (HESK-) HESKA CORP.
 PA

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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 20.33 Seconds

(without alignments)
441.856 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288
Sequence: 1 LNTTTLTPNGNEDT7ADPFL.....QHNSKSPHFHNGSTSKEN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1388	100.0	369	1 CYRG_HUMAN	P31785 homo sapien
2	1097	85.2	373	1 CYRG_CANFA	P40321 canis fam11
3	990.5	76.9	379	1 CYRG_BOVIN	Q95182 bos taurus
4	853.5	66.3	369	1 CYRG_MOUSE	P34902 mus musculu
5	207	16.1	380	1 I132_HUMAN	Q14627 homo sapien
6	181.5	14.1	424	1 I131_MOUSE	Q09030 mus musculu
7	178	13.8	427	1 I131_HUMAN	P78552 homo sapien
8	159	12.3	897	1 CYRB_HUMAN	P32927 homo sapien
9	150	11.6	831	1 PRIR_CHICK	Q04594 gallus gall
10	146.5	11.4	400	1 GPCR_HUMAN	P15504 homo sapien
11	145.5	11.3	831	1 PRIR_MELGA	Q91094 melalegris g
12	132.5	10.3	830	1 PRIR_COLLI	Q90374 columba liv
13	132	10.2	810	1 I14R_MOUSE	P16382 mus musculu
14	125	9.7	896	1 CYRB_MOUSE	P26955 mus musculu
15	121.5	9.4	581	1 PRIR_BOVIN	Q28172 bos taurus
16	118	9.2	415	1 I15R_MOUSE	P22173 mus musculu
17	116	9.0	878	1 I13B_MOUSE	P26954 mus musculu
18	114	8.9	460	1 I16A_MOUSE	P22272 mus musculu
19	113	8.8	581	1 PRIR_CEREL	Q02823 cervus elap
20	112	8.7	420	1 I15R_HUMAN	Q01344 homo sapien
21	112	8.7	918	1 I16B_HUMAN	P40189 homo sapien
22	110.5	8.6	551	1 I12B_HUMAN	P14784 homo sapien
23	109.5	8.5	608	1 PRIR_MOUSE	Q08501 mus musculu
24	109	8.5	462	1 I16A_RAT	P22273 rattus norv
25	108.5	8.4	610	1 PRIR_RAT	P05710 rattus norv
26	105	8.2	539	1 I12B_MOUSE	P16297 mus musculu
27	105	8.2	1356	1 CA21_ONCMY	Q93484 oncorhynch
28	104.5	8.1	917	1 I16B_MOUSE	Q00560 mus musculu
29	104	8.1	1493	1 NEOL_MOUSE	P97398 mus musculu
30	102	7.9	611	1 GHR_COLLI	Q90375 columba liv
31	98.5	7.6	918	1 I16B_RAT	P40190 rattus norv
32	97.5	7.6	467	1 I16A_PIG	O18796 sus scrofa
33	97.5	7.6	608	1 GHR_CHICK	Q00092 gallus gall

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	369 AA.
CYRG_HUMAN				
AC P31785;				
DT 01-JUL-1993 (Rel. 26, Created)				
DT 01-JUL-1993 (Rel. 26, Last sequence update)				
DT 16-OCT-2001 (Rel. 40, Last annotation update)				
DE Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64) (CD132 antigen).				
GN I12RG.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX MEDLINE=92355883; PubMed=1631559;				
RA Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,				
RA Munakata H., Nakamura M., Sugamura K.;				
RT "Cloning of the gamma chain of the human IL-2 receptor.";				
RL Science 257:379-382(1992).				
RN [2]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=93293887; PubMed=8514792;				
RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;				
RT "Characterization of the human Interleukin-2 receptor gamma chain gene.";				
RL J. Biol. Chem. 268:13601-13608(1993).				
RN [3]				
RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.				
RX MEDLINE=94004847; PubMed=8401490;				
RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,				
RA Willard H., Henthorn P.S.;				
RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked severe combined immunodeficiency, SCID1.";				
RL Hum. Mol. Genet. 2:1099-1104(1993).				
RN [4]				
RP IDENTIFICATION AS A IL-4R SUBUNIT.				
RX MEDLINE=94090315; PubMed=8266076;				
RA Rondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,				
RA Arai K.-I., Sugamura K.;				
RT "Shaping of the interleukin-2 (IL-2) receptor gamma chain between receptors for IL-2 and IL-4.";				
RL Science 262:1874-1877(1993).				
RN [5]				
RP IDENTIFICATION AS A IL-4R SUBUNIT.				
RX MEDLINE=94090317; PubMed=8266078;				
RA Russell S.M., Kkegan A.D., Harada N., Nakamura Y., Noguchi M.,				
RA Leonard P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,				
RT "Interleukin-2 receptor gamma chain: a functional component of the Interleukin-4 receptor.";				
RL Science 262:1880-1883(1993).				
RN [6]				
RP IDENTIFICATION AS A IL-7R SUBUNIT.				

34	97.5	7.6	825	1 I14R_HUMAN	P24394 homo sapien
35	96.5	7.5	625	1 TPOR_MOUSE	Q08351 mus musculu
36	95.5	7.4	622	1 PRIR_HUMAN	P16471 homo sapien
37	95.5	7.4	630	1 PRIR_ORENI	Q91513 oreochromis
38	95.5	7.4	1461	1 NEOL_HUMAN	Q92859 homo sapien
39	95	7.4	312	1 F3ST_FLABI	P52835 flavaria bl
40	93	7.2	537	1 I12B_RAT	P26896 rattus norv
41	92.5	7.2	1282	1 DOME_DROME	Q9VWE0 drosophila
42	92	7.1	508	1 EPOR_HUMAN	P19235 homo sapien
43	91.5	7.1	507	1 EPOR_MOUSE	P14753 mus musculu
44	91.5	7.1	1443	1 NEOL_CHICK	Q90610 gallus gall
45	91.5	7.1	1630	1 PRPL_DROME	P35992 drosophila

RX MEDLINE-94090316; PubMed-8266077;
 RA Noguuchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT Interleukin-7 receptor";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE-95111955; PubMed-7529123;
 RA Bamorough P., Heggecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANT XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE-94130970; PubMed-829698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE-94375038; PubMed-8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCIDX1 that
 RT differentially affect the mRNA processing";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE-94300093; PubMed-8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Kono T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency";
 RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE-95023932; PubMed-7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]
 RP VARIANT XSCID CYS-226 AND HIS-226.
 RX MEDLINE-95397841; PubMed-7688284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE-96013903; PubMed-7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levisky R.L., Kinon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE-95164726; PubMed-7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma chain mutation causing X-linked severe combined
 RT immunodeficiency";
 RL J. Clin. Invest. 95:895-899(1995).

RN [15]
 RP VARIANT XSCID GLN-293.
 RX MEDLINE-95190013; PubMed-7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguuchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE-97042245; PubMed-8900089;
 RA Stephan V., Mann V., Le Deist F., Dirksen U., Broecker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE-97295088; PubMed-9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE-98064061; PubMed-9399950;
 RA Sharif N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE
 CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -1- DATABASE: NAME=PROIM; NOTE=CD guide cd132 entry.
 CC WWW="http://www.ncbi.nlm.nih.gov/proc/cd/cd132.htm".
 CC -1- DATABASE: NAME=IL2RGbase; NOTE=X-linked SCID mutation database;
 CC WWW="http://www.nhgri.nih.gov/DIR/GMIB/SCID/".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D11086; BAA01857.1; -;
 DR EMBL: L12183; AAA59145.1; -;
 DR EMBL: L12178; AAA59145.1; JOINED.
 DR EMBL: L12176; AAA59145.1; JOINED.
 DR EMBL: L12177; AAA59145.1; JOINED.
 DR EMBL: L12179; AAA59145.1; JOINED.
 DR EMBL: L12180; AAA59145.1; JOINED.
 DR EMBL: L12181; AAA59145.1; JOINED.
 DR EMBL: L12182; AAA59145.1; JOINED.
 DR EMBL: L12182; AAA59145.1; JOINED.
 DR EMBL: L19546; AAC37524.1; -;
 DR PIR: A42565; A42565.
 DR PDB: 1ILM; 26-JAN-95.
 DR PDB: 1ILN; 26-JAN-95.
 DR MIM: 308380; -;
 DR MIM: 300400; -;
 DR InterPro: IPR002996; CRLA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.

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 DR EMBL: U33748; AAB07812.1; -
 DR HSSP: P31785; IILN.
 DR InterPro: IPR002936; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; fn3; 1.
 DR PROSITE: PS01355; Hematopo_REC_S_F1; 1.
 DR Receptor: Transmembrane; Glycoprotein; Signal.
 KM SIGNAL: 1 22
 FT CHAIN: 23 379
 FT DOMAIN: 23 269
 FT TRANSMEM: 270 290
 FT DOMAIN: 291 379
 FT DOMAIN: 158 256
 FT DISULFID: 109 122
 FT DISULFID: 77 77
 FT CARBOHYD: 81 81
 FT CARBOHYD: 90 90
 FT CARBOHYD: 166 166
 FT CARBOHYD: 171 171
 SQ SEQUENCE 379 AA: 43037 MW: 336FAD9C9B032178 CRC64:
 Query Match 76.9%; Score 990.5; DB 1; Length 379,
 Best Local Similarity 76.2%; Pred. No. 1.4e-76;
 Matches 182; Conservative 21; Mismatches 29; Indels 7; Gaps 2;
 QY 1 LNTTILTPNGNED-----TTAEFLTPMTDLSYSTLPLEVOCEFNVEYKNCNTNS 54
 Db 23 LNKREFLPSNEDIGKPGTSGDFILSTPAGLDVSTLPKVCQCFVAVNYKNCNTNS 82
 QY 55 GSEBPQNLTLHYWKYK-SDNKKVQKSHYLSSEETSCQLOKKEIHLVQFFVQLODP 113
 Db 83 GSEBPQNLTLHYGKRFNFGDDKLCGCHYLFSEGITSCGKFGKEIRLYETFFVQLODP 142
 QY 114 REPRRQATQWLKLTQNYIPAPENLTLHKLSQSLAMNNRFLNCHLEHLYQFFVQMDH 173
 Db 143 REHKQKQKMLKLDVLIIPAPENLTLRNLSERQLELSMKNYLDHCLHLYQVYSRDR 202
 QY 174 SMTBQSYDYHKKFSLPSVDGQKRYTFRVSRNPCLGSAQHMSNSHPILHMSNTSKEN 232
 Db 203 SMTBQSYDYHKKFSLPSVDGQKRYTFRVSRNPCLGSAQHMSNSHPILHMSNTSKEN 261
 RESULT 4
 CYRG_MOUSE STANDARD; PRT; 369 AA.
 AC P34902;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277575; PubMed=8503926;
 RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.,
 RT "Cloning of the mouse interleukin 2 receptor gamma chain:
 RT demonstration of functional differences between the mouse and human
 RT receptors.";
 RL Blochem. Biophys. Res. Commun. 193:356-363(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/CA;
 RX MEDLINE=93391374; PubMed=8378320;
 RX Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
 RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
 RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
 RT IL-2R gamma chain expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9336191; PubMed=8359699;
 RA Kobayashi N., Nakagawa S., Mimami Y., Taniguchi T., Kono T.;
 RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
 RT gamma.";
 RL Gene 130:303-304(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95104285; PubMed=7805729;
 RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
 RA Fischer A., de Saint Basile G.;
 RT "The murine interleukin-2 receptor gamma chain gene: organization,
 RT chromosomal localization and expression in the adult thymus.";
 RL Eur. J. Immunol. 24:3014-3018(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S;
 RX MEDLINE=96341745; PubMed=8750189;
 RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
 RA Dougherty G.J.;
 RT "Molecular mechanisms regulating the hyaluronan binding activity of
 RT the adhesion protein CD44.";
 RL J. Neurosci. 26:231-239(1995).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 DR EMBL: D13821; BAA02974.1; -
 DR EMBL: U21795; AAA64279.1; -
 DR EMBL: D13565; BAA02760.1; -
 DR EMBL: L20048; AAA39286.1; -
 DR EMBL: S75852; AAB32904.1; -
 DR EMBL: S75844; AAB32904.1; JOINED.
 DR EMBL: S75845; AAB32904.1; JOINED.
 DR EMBL: S75847; AAB32904.1; JOINED.
 DR EMBL: S75848; AAB32904.1; JOINED.
 DR EMBL: S75849; AAB32904.1; JOINED.
 DR EMBL: S75850; AAB32904.1; JOINED.
 DR EMBL: S75851; AAB32904.1; JOINED.
 DR EMBL: X75337; CAA53085.1; -
 DR PIR: JN0592; JN0592.
 DR PIR: JN0775; JN0775.
 DR HSSP: P31785; IILN.
 DR MGD: MGI:96551; IL2rg.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; fn3; 1.
 DR PROSITE: PS01355; Hematopo_REC_S_F1; 1.
 KM Receptor: Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22
 BY SIMILARITY.

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FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284 POTENTIAL.
FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
FT DISULFID 151 250 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT CARBOHYD 102 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;

```

Query Match 66.3%; Score 853.5; DB 1; Length 369;
 Best local similarity 67.2%; Pred. No. 4,9e-65;
 Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

```

2 NTFILTPNGEDTADFEITMPDLSVSTPLPEVOCFVFNRYMCTWNSSEPOPT 61
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
24 SSKVLMSSANEDIKADLITSTAPEHLSATPLPEVOCFVFNRYMCTWNSSEPOAT 83
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 NLTLYHWKNSDNDKVKCSHYLFSEETISGCOLKKEIHLVYQTFVVOLODPREPRQAT 121
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
84 NLTLYHWKNSDNDKVKCSHYLFSEETISGCOLKKEIHLVYQTFVVOLODPREPRQAV 143
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 OMKLQNLVTPWAPENLTPLKLSQSDELMMNRP--NHCLHLYVQTFVVOLODPREPRQAT 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
144 OKNLQNLVTPWAPENLTPLKLSQSDELMMNRP--NHCLHLYVQTFVVOLODPREPRQAT 203
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 DDKHRSKLSVYDGRKRYFRVRSRFPFLGSAQHSSEMSHPHMSNSKRN 232
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
204 NHPRRSLSVYDGRKRYFRVRSRFPFLGSAQHSSEMSHPHMSNSKRN 255

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RESULT 5
ID 1132_HUMAN STANDARD; PRT; 380 AA.
AC Q14627; 000667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13
  binding protein).
GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=8663118;
RA Caput D., Laurent P., Kagnad M., Lelias J.M., Lefort S., Vita N.,
  Ferrara P.;
RT "Cloning and characterization of a specific interleukin (IL)-13
  binding protein structurally related to the IL-5 receptor alpha
  chain."
RT J. Biol. Chem. 271:16921-16926(1996).
RL [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D., Whiters M.J., Fitz L., Neben T., Flinnerty H.,
  Henderson S.L., O'Hara R.M., Jr., Turner K.J., Wood C.R., Collins M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J., Aptou F., Meillerin M.P., Lebeau B., Jacques Y., Minvielle S.;
RT Chromosome mapping and expression of the human Interleukin-13

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RT receptor."
RL Genomics 42:141-145(1997).
CC -1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13
  (IL-13), BUT NOT TO IL-4.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; X95302; CA664617.1; -
DR EMBL; Y07981; AAB17170.1; -
DR EMBL; Y08768; CAA70021.1; -
DR MIM; 300130; -
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR Pfam; PF00041; fn3_1.
DR PROSITE; PS0156; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN.
FT DOMAIN 27 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 363 POTENTIAL.
FT DOMAIN 364 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 145 155 BY SIMILARITY.
FT DISULFID 184 197 BY SIMILARITY.
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B552C887 CRC64;

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Query Match 16.1%; Score 207; DB 1; Length 380;
 Best local similarity 25.4%; Pred. No. 2e-10;
 Matches 60; Conservative 46; Mismatches 106; Indels 24; Gaps 9;

```

9 NNGEDTTADFEITMPDLSVSTPLPEVOCFVFNRYMCTWNSSEPOPT-----T 61
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
115 NGSE-VQSMATTYWISPGIPEYKQDMCYVYIMQYLCSW-----KPGIVILDT 167
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 NLTLYHWKNSDNDKVKCSHYLFSEETISGCOLKKEIHLVYQTFVVOLODPRE--PRQ 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
168 NNYLFWYEGDGH--ALQCVYIKADQNTGCFPYLEASDKRDFYICVNGSSENKPIRS 225
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 ANQMLKQNLVTPWAPENLTPLKLSQSDELMMN--NHCLHLYVQTFVVOLODPRE 176
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
226 SYTFQQLQIVKLPFPYVLPPTRESSEIKLWSILPGIPARCVDYIELRED-DITLV 284
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 EOSVDYRHKFSIPSYDGRKRYFRVRSRFPFLGSAQHSSEMSHPHMSNSKRN 231
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
285 TAIVE-NETIYIKTINERQLCFVRSKVIYICSDGIGTSEMSKQCKWEGEDLSK 339
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 6
ID 1131_MOUSE STANDARD; PRT; 424 AA.
AC D09030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
  13RA-1) (Interleukin-13 binding protein) (NR4).
GN IL13RA1 OR IL13R OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


EMBL: U81379; AAD00510.3; -
 DR HSSP; P40189; IBCU.
 DR MIM; 300119; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 427 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
 FT DOMAIN 22 343 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 344 367 POTENTIAL.
 FT DOMAIN 368 427 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 102 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 46 95 POTENTIAL.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 173 185 BY SIMILARITY.
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 130 130 T -> I (IN REF. 3).
 FT CONFLICT 358 358 G -> D (IN REF. 3).
 SQ SEQUENCE 427 AA; 48759 MW; 5983B3BF54107B CRC64;

Query Match 13.8%; Score 178; DB 1; Length 427;
 Best Local Similarity 26.7%; Pred. No. 6.4e-08;
 Matches 58; Conservative 38; Mismatches 83; Indels 38; Gaps 11;

OY 37 EVQCFVNEVYKNTWSSSEPQ-TNLTLYWYKNSDNDKYOKSHYLFSEETISGC-- 93
 DB 131 ELQCIIMHNSLYKMSGLPGRTSPPTNTLYLVYHRSI--EKIHQEN-IPREGQFGGSF 187
 OY 94 QLOKKEIHLVQTFVQVL--QDPRPRQATOMLKLQNLVTPWAP--ENULTLHKISESOLE 149
 DB 188 DLTLYKDSSEFQHSVOIWKKNAGKIKSFNIVPLTSHKVDPPRIKMSFH--NDLXL 244
 OY 150 LNMWN--RELNHCLEHLVQRTMDHNSWT-----DQSDYRHKESLP 189
 DB 245 VQMEHPQNFISKCL----FYEYEVNNSQTEHNVFYVOEAKCENPEFERNVENTSCFVWP 300
 DB 301 GVLPTLMTVTRIRVKTNKLCTYEDDKLMSNGSEMSIG 337
 RESULT 8
 CYRB_HUMAN STANDARD; PRT; 897 AA.
 ID CYRB_HUMAN P32927;
 AC 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytokine receptor common beta chain precursor (CDW131 antigen).
 GN CSF2RB OR IL3RB OR IL3RB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91088571; PubMed=1702217;
 RA Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
 Miyajima A.;
 RT Molecular cloning of a second subunit of the receptor for human

RT granulocyte-macrophage colony-stimulating factor (GM-CSF);
 RT reconstitution of a high-affinity GM-CSF receptor";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
 RN [2]
 RP REVISION TO 454.
 RA Kitamura T.;
 RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide cdw131 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw131.htm".
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL; M59941; AAA18171.1; -
 DR PIR; A39255; A39255.
 DR HSSP; P19325; 1EBA.
 DR MIM; 138981; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL 1 16
 FT CHAIN 17 897 CYTOKINE RECEPTOR COMMON BETA CHAIN.
 FT DOMAIN 17 443 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 444 460 POTENTIAL.
 FT DOMAIN 461 897 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 129 238 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 336 434 FIBRONECTIN TYPE-III 2.
 FT DISULFID 35 45 BY SIMILARITY.
 FT DISULFID 75 91 BY SIMILARITY.
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 897 AA; 97335 MW; 3398E37FDB8F393A CRC64;

Query Match 12.3%; Score 159; DB 1; Length 897;
 Best Local Similarity 26.4%; Pred. No. 6.4e-06;
 Matches 55; Conservative 40; Mismatches 79; Indels 34; Gaps 12;

OY 38 VOCFVNEVYKNTWSSSEPQTNLTLYWYKNSDNDKYOKS---HYLFSEETISGC 93
 DB 248 LECFFDAVAIVSCSWERKE-VASSVSFGLFKPSDPAGEEESPVLRBGLSLRRHNC 306
 OY 94 QLOKKEIHLVQTFVQVLQDPRPRQATOMLKLQNLVTPWAPENULTLHKISESOLEANN 153
 DB 307 QIIPDPATHGQYIVSQ---PRR-AEKIKK-SSVNIQWAPSLVNTKDGDS-YSLRME 359
 OY 154 NRELNHCLEHL-----VQRTD---WDHSWTEQSDYRHKESLPVSDGQKRTYFRKSR 204
 DB 360 TMRKRY--EHIDHTEFLQYRKDTATWDSKTE-TLQNAHSMALPALEPSTRYWARVRRT 416
 OY 205 ----FNPLCSAQHSWSESHPIHMSNT 228
 DB 417 SRIGYNGI-----WSEWSEARSDTES 438

```

RESULT 9
PRLR.CHICK STANDARD: PRT: 831 AA.
AC 004594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
RN NCBI_TaxId=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
"Double antenna structure of chicken prolactin receptor deduced from
the cDNA sequence.";
Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: D13154; BAA02439.1; -
DR PIR: JQ1655; JQ1655.
DR HSSP: P14787; IAN3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; FN3_4.
DR SMART: SM00060; FN3_3.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1_1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
FT CARBOHYD 335 335
FT SEQUENCE 831 AA; 94102 MW; 1CAE75791DCADBE9 CRC64;
Query Match 11.6%; Score 150; DB 1; Length 831;
Best Local Similarity 25.0%; Pred. No. 3.4e-05;
Matches 50; Conservative 34; Mismatches 90; Indels 26; Gaps 9;

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OY 38 VOCEFEVNEVMNCWNSNSE--POPTNLTLHYKNKSDNDKVCXSHLYFSEITSG---C 93
DB 34 ITRSLKETETSCWKKPSSDGLPTNNTL--FYKSDSEETIECPDR-----ISGNSC 86
OY 94 OLQKKEIHLVQYTFVYQLODPREPRRQAT--OMLKQNLVTPWADENLTIL-KISEQLEL 150
DB 87 YFNKHTSPMTTFNTITVATNEICSSNSDPQYDVNTSVPGSGVNLTLTKRSANIMYL 146
OY 151 --NMNRRFL-----NHCEHLVQYRTDWDHSTQSDVYRHKEFLSPYDQCKRTYFVR 203
DB 147 WAKWSPPLLDASSNHLHYELRIKPEKEEMETISVGVOYCKINRLNMGMRIVQVRC 206
OY 204 RFPNPGSGSAOHSEWSEHPH 223
DB 207 TLDP-----GEMSEWSESRH 221

RESULT 10
GMCR_HUMAN STANDARD: PRT: 400 AA.
AC P15509; 014429; 014430; 014431; 000207; Q16564;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor receptor alpha
DE chain precursor (GM-CSF-R-alpha) (GMR) (CD116) (CD116 antigen).
GN (CSF2RAX OR CSF2RA OR CSF2R OR CSF2RX) AND
GN (CSF2RAY OR CSF2RA OR CSF2R OR CSF2RY).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=90059966; PubMed=2555171.
RA Gearing D.P., King J.A., Gough N.M., Nicola N.A.;
"Expression cloning of a receptor for human granulocyte-macrophage
RT colony-stimulating factor.";
EMBO J. 8:3667-3676(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=94193800; PubMed=8144676;
RA Nakagawa Y., Kosugi H., Miyajima A., Arai K.I., Yokota T.;
"Structure of the gene encoding the alpha subunit of the human
RT granulocyte-macrophage colony stimulating factor receptor.
RT Implications for the evolution of the cytokine receptor
RT superfamily.";
J. Biol. Chem. 269:10905-10912(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=91352066; PubMed=1715577;
RA Crosier K.E., Wong G.G., Mathey-Prevet B., Nathan D.G., Steff C.A.;
"Cloning of a potentially soluble receptor for human GM-CSF.";
Nucleic Acids Res. 18:7178-7178(1990).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Placenta;
RX MEDLINE=91088339; PubMed=2148207;
RA Ashworth A., Kraft A.;
"Cloning of a potentially soluble receptor for human GM-CSF.";
Nucleic Acids Res. 18:7178-7178(1990).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=91376112; PubMed=1832774;
RA Raines M.A., Liu L., Qian S.G., Joe V., DiPersio J.F., Golde D.W.;
"Identification and molecular cloning of a soluble human granulocyte-
RT macrophage colony-stimulating factor receptor.";
Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
RC TISSUE=Blood;

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RX MEDLINE=94368898; PubMed=8086503;
 RA Hu X., Emanuel P.D., Zuckerman K.S.;
 RT "Cloning and sequencing of the cDNA encoding two alternative
 RT splicing-derived variants of the alpha subunit of the granulocyte-
 RT macrophage colony-stimulating factor receptor.";
 RL Blochim. Biophys. Acta 1223:306-308(1994).
 RN [7].
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RA Hu X., Zuckerman K.S.;
 RT "Cloning and sequencing of the cDNA variant with 397 bp missing
 RT for the GM-CSF receptor alpha subunit.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-
 CC STIMULATING FACTOR. TRANSDUCES A SIGNAL THAT RESULTS IN THE
 CC PROLIFERATION, DIFFERENTIATION, AND FUNCTIONAL ACTIVATION OF
 CC HEMATOPOIETIC CELLS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN. ISOFORMS 3, 4 AND 6
 CC ARE PROBABLY SOLUBLE.
 CC -1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4, 5 AND
 CC 6: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: X17648; CA55638.1; -;
 DR EMBL: D26628; BAA05656.1; -;
 DR EMBL: D26618; BAA05656.1; JOINED.
 DR EMBL: D26619; BAA05656.1; JOINED.
 DR EMBL: D26620; BAA05656.1; JOINED.
 DR EMBL: D26621; BAA05656.1; JOINED.
 DR EMBL: D26622; BAA05656.1; JOINED.
 DR EMBL: D26623; BAA05656.1; JOINED.
 DR EMBL: D26624; BAA05656.1; JOINED.
 DR EMBL: D26625; BAA05656.1; JOINED.
 DR EMBL: D26626; BAA05656.1; JOINED.
 DR EMBL: D26627; BAA05656.1; JOINED.
 DR EMBL: M64445; AAA35908.1; -;
 DR EMBL: X54935; CA538697.1; -;
 DR EMBL: M73832; AAA35909.1; -;
 DR EMBL: L29348; AAA60961.1; -;
 DR EMBL: L29349; AAA60962.1; -;
 DR EMBL: U93096; AAB51535.1; -;
 DR PIR: S06945; S06945.
 DR MIM: 306250; -;
 DR MIM: 425000; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; signal; Alternative splicing.
 FT SIGNAL 1 22
 FT CHAIN 23 400
 FT DOMAIN 23 320
 FT TRANSMEM 321 346
 FT DOMAIN 347 400
 FT DISULFID 126 136
 FT DISULFID 165 178
 FT CARBOHYD 46 46
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 123 123
 FT CARBOHYD 135 135
 FT CARBOHYD 182 182
 FT CARBOHYD 195 195
 FT CARBOHYD 223 223

FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 216 233 ERNPPSNVYRNTTHC -> GSLTSGCSRFHNSKTN
 FT VARSPPLIC 234 400 MISSING (IN ISOFORM 6).
 FT VARSPPLIC 271 286 MISSING (IN ISOFORM 6).
 FT VARSPPLIC 287 400 INVSGLDENYRNPSS -> VVLTSTALCTFMS (IN
 FT VARSPPLIC 316 400 ISOFORM 4).
 FT VARSPPLIC 318 333 GSDGNIGSYTYIVLLVGLVGLVGLFRRRLQRLF
 FT VARSPPLIC 334 400 PPVQIDKRLNDHEVEDETIMEEFPEEGKGRREVLTK
 FT VARSPPLIC 376 400 EIT -> DMLGIGHRGRRLPRGLDREGNLRRCGRN
 FT SEQUENCE 400 AA; 46206 MW; D9025B91E41311D CRC64; GMDISASATGNCFLDVAIVLYIIFYVFI (IN ISOFORM
 5).
 Query Match 11.4%; Score 146.5; DB 1; Length 400;
 Best Local Similarity 21.1%; Pred. No. 2.7e-05;
 Matches 52; Conservative 44; Mismatches 90; Indels 61; Gaps 10;
 QY 5 ILTFN-GNEDTADFLITMPTDLSVTLPLPVQCFVFNVEVMNTMSSSPQPTNL 63
 DB 109 LLYVNSGREGTAQNF-----SCETYNADIMCTW-ARQPTAPRV 148
 QY 64 TLHWYKNSDNKDYQKCSHYLFSEITSGCOLQ-----KKEIHLVQTFV 107
 DB 149 QYFLYINRSKRREIRCPYIQQDSCTHVGCHLDLSGLTSRNFVNGTIREIGI -QFF 206
 QY 108 VOLDDPRE-----PRQATQMLKQLNIVIPAPENITLHLS--ESQLEIMNNRFLNHC 160
 DB 207 DSLDFTKKIERFNPSPSVTVACNTTHCLVHW-KOPRTYKLTSLDIPQYQDLVHRKKTQPG 265
 QY 161 LEHLYOYRTDMDHSWTQSDVYRHKFSLPSVDGKRTFVRSFNFLCQSAHWSEMSH 220
 DB 266 TENLL-----INVSGLDENRYNPPSEPPAKHSVKIRADVRLT---NWSWSSE 311
 QY 221 PIHWGNS 227
 DB 312 AIEFGSD 318
 RESULT 11
 PRLR_MELGA STANDARD; PRT; 831 AA.
 AC 091094; 091091; 091092;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (TPRLR).
 GN PRLR.
 OS Meleagris gallinavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_Taxid=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97057891; PubMed=8902221;
 RA Zhou J.F., Zadororny D., Guemene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RL gallinavo.";
 RL Biol. Reprod. 55:1081-1090(1996).
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE=Ovary;
 RA Pits G.R., You S.K., Foster D.N., el Halawani M.E.;


```

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -i FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -i SUBCELLULAR LOCATION: Type I membrane protein.
CC -i SIMILARITY: BELONGS TO THE CYTOKINE FAMILY III-LIKE DOMAINS.
CC -i SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L76587; AAB01544.1; -
DR EMBL: U22947; AAB75038.1; -
DR EMBL: U22924; AAB75039.1; -
DR HSSP: P16471; IBP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94394 MM; 220916320F77FAC1 CRC64;

Query Match 11.3%; Score 145.5; DB 1; Length 831;
Best Local Similarity 24.3%; Pred. No. 8e-05;
Matches 53; Conservative 36; Mismatches 94; Indels 35; Gaps 10;

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AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic Pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=9932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CropSac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horsman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RL receptor.";
RL Endocrinology 135:269-276(1994).
CC -i FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -i SUBCELLULAR LOCATION: Type I membrane protein.
CC -i SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -i SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL: U07694; AAA20646.1; -
DR HSSP: P16471; IBP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 440 460
FT DOMAIN 461 830 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 226 FIBRONECTIN TYPE-III 2.
FT DOMAIN 229 326 FIBRONECTIN TYPE-III 3.
FT DOMAIN 327 429 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 830 AA; 94507 MM; 3B074E83CDE69E9F CRC64;

Query Match 10.3%; Score 132.5; DB 1; Length 830;
Best Local Similarity 22.2%; Pred. No. 0.001;
Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;

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Db 90 KNTNTWMTYNTYNTVMAMNELGSSNDPOYVDYTSIQPAPNLSLEFRTSASTYTLAK 149
Qy 152 WNNRFL-----NHCLEHLVQRTMDHSMTEOSVDYRHKESLPSYDGOKRTYFRVSRF 205
Db 150 WSPPLADYTSNHYVRYELRLKPEKEEMETVYSGVQYQVKNRLQAGKVVQVRCVL 209
Qy 206 NPLGSAQHSEWSHPH 223
Db 210 D-----IGEMSEWSSERH 222

RESULT 13
IL4R MOUSE STANDARD: PRT: 810 AA.
AC P16382;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
SE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha).
IL4R OR IL4RA
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 26-39; 162-179 AND 194-210.
RX MEDLINE=90030408; PubMed=2805066;
RA Mostly B., Beckmann M.P., March C.J., Idzerda R.L., Gimpel S.D.,
RA Vandenbos T., Friend D., Alpert A., Anderson D., Jackson J.,
RA Mignall J.M., Smith C., Gallis B., Slins J.E., Urdal D., Widmer M.B.,
RA Cosman D., Park L.S.;
RT "The murine interleukin-4 receptor: molecular cloning and
RT characterization of secreted and membrane bound forms.";
RL Cell 59:335-348(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90138976; PubMed=2405398;
RA Harada N., Castile B.E., Gorman D.M., Itoh N., Schreurs J.,
RA Barrett R.L., Howard M., Miyajima A.;
RT "Expression cloning of a cDNA encoding the murine interleukin 4
RT receptor based on ligand binding.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:857-861(1990).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-4. THE SOLUBLE FORM
CC FOR THE IL-4 RECEPTOR MAY REPRESENT A REGULATORY MOLECULE SPECIFIC
CC FOR IL-4 DEPENDENT IMMUNE RESPONSES.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: THERE ARE THREE CLASSES OF IL-4 RECEPTOR:
CC ONE CONTAINING EXTRACELLULAR, TRANSMEMBRANE, AND CYTOPLASMIC
CC DOMAINS, A SECOND LACKING THE CYTOPLASMIC DOMAIN, AND A THIRD
CC BEING A SECRETED FORM OF THE RECEPTOR. ALL THREE BIND IL-4.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: M27959; AAA39299.1; -
DR EMBL: M27960; AAA39300.1; -
DR EMBL: M29854; AAA39297.1; -
DR PIR: A33380; A33380.
DR MGD; MGI:105367; Il4ra.
DR InterPro: IPR002966; CRLA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003531; Hematopo_receptor_S_FL.
DR Pfam: PF00041; fn3.1.
DR PROSITE: PS01355; HEMATOPO_REC_S_FL; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.

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FT SIGNAL 1 25
FT CHAIN 26 810 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
FT DOMAIN 26 233 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 234 257 POTENTIAL.
FT DOMAIN 258 810 CYTOPLASMIC (POTENTIAL).
FT DISULFID 34 44 BY SIMILARITY.
FT CARBOHYD 75 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 225 230 HFQPLP -> PSNENL (IN SECRETED ISOFORM).
FT VARSPPLIC 231 810 MISSING (IN SECRETED ISOFORM).
FT VARSPPLIC 258 810 MISSING (IN THIRD ISOFORM).
SQ SEQUENCE 810 AA; 87627 MW; 53699E01E938FE6D CRC64;

Query Match 10.2%; Score 132; DB 1; Length 810;
Best Local Similarity 26.2%; Pred. No. 0.0011;
Matches 60; Conservative 28; Mismatches 107; Indels 34; Gaps 8;

Qy 14 TTADFLLTMTPLDISVSTPLPEVOCFVNEVEMNCTW--NSSEPPITNLTHYWKNS 72
Db 10 TSVGCLILLVYTGSGSIRKVGEP--TCFSXYIRTSGEMFLDSAVDCSSQLCHY----- 62
Qy 73 DNDKQKCSHYLFSEET-----SGCOLKKEIHLQYTFVQLODPREPRROATQML 124
Db 63 -----RLMFEFESNLTICIRNSASTYVCCHMEMNRPVSDRQMLMEHRQLMQSGF 116
Qy 125 KLQNLVFWAPENLTILKLSQELMNNRFLNHC-L-EHLVQY----RTMDHSMTEQ 178
Db 117 SPSSGKPLPADNLTILHNVSDEWLTWNLYPSNNLKYKLKLVNINISBDNPAEPIYV 176
Qy 179 SVDY---RHKESLPSYDGOKRTYFRVRSFENPLGSAQHSEWSHPH 224
Db 177 NTVKPEPLSPFINITLMGCVYITARVRSQILIGT---MSWSPSITW 222

RESULT 14
CYRB MOUSE STANDARD: PRT: 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common beta chain precursor.
GN CSF2RB OR CSF2RB1 OR AIC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----

DR EMBL: M34397; AAA37204.1; -

DR PIR: A35782; A35782.

DR MGD: MG1:1339759; Csf2rb1.

DR Interpro: IPR002996; CRIA.

DR Interpro: IPR00282; Cytok_receptor_2.

DR Interpro: IPR003961; FN.III.

DR Interpro: IPR003531; Hematopo_receptor_S.Fl.

DR Pfam: PF00041; fn3; 2.

DR PROSITE: PS01355; HEMATOPO_REC_S.Fl; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 896

FT DOMAIN 23 441

FT TRANSMEM 442 463

FT DOMAIN 464 896

FT DOMAIN 132 241

FT DOMAIN 343 440

FT DISULFID 39 49

FT CARBOHYD 62 62

FT CARBOHYD 141 141

FT CARBOHYD 350 350

FT SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A999 CRC64;

Query Match 9.7%; Score 125; DB 1; Length 896;

Best Local Similarity 23.1%; Pred. No. 0.0047; Mismatches 82; Indels 42; Gaps 11;

Matches 48; Conservative 36; Mismatches 82; Indels 42; Gaps 11;

QY 38 VOCFVFNVEYMCNTMNSSEPPPTNLTLYWYKNSDNDKVKCSHYLFSEETSGCLOK 97

DB 251 LQCFEFDIGSLHCSWEVWQ-TGVSFGLFPRSPVAPBEKSPVY----- 296

QY 98 KE---IHLVOTFYVQLODRPREPROATOMIKLONLV-----IPAPENLILHKL 144

DB 297 KPPGASVYTRYHCSLPVP-EPSSHSQYTVSVKHLQGFINSYNIHQEPPLNLTNR 355

QY 145 ESOLELMMNMR-----FLNCHLEHLVQYR---TDMDSMTQESVDYRHKFSLPSVDGQR 196

DB 356 DS-YSLHWETQKMAYSFIETFP--VOYKKKSDSWEDSKTE-NLDNAHMDLSQLEPDT 411

QY 197 YTFVRNSRPNLCGSAOHSEMSHPITW 224

DB 412 YCARVHYK--PISNYDGIWSKWESEYTW 437

SUPT 15

PRLR_BOVIN

ID PRLR_BOVIN STANDARD; PRT; 581 AA.

AC 028172;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Prolactin receptor precursor (PRL-R).

GN PRLR.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Endometrium;

RX MEDLINE=93246019; PubMed=1338725;

RA Scott P., Kessler M.A., Schuler L.A.;

RT "Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues";

RL Mol. Cell. Endocrinol. 89:47-58(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

CC PROLACTIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----

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CC -----

DR EMBL: L02549; AAA51417.1; -

DR HSSP: P14787; IAN3.

DR Interpro: IPR002996; CRIA.

DR Interpro: IPR003961; FN.III.

DR Interpro: IPR003528; Hematopo_receptor_L.Fl.

DR Pfam: PF00041; fn3; 2.

DR SMART: SM00060; FN3; 2.

DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 24

FT CHAIN 25 581

FT DOMAIN 25 234

FT TRANSMEM 235 258

FT DOMAIN 259 581

FT DOMAIN 123 227

FT DISULFID 36 46

FT CARBOHYD 59 59

FT CARBOHYD 132 132

FT SEQUENCE 581 AA; 65153 MW; 7385C0D6956EBE139 CRC64;

Query Match 9.4%; Score 121.5; DB 1; Length 581;

Best Local Similarity 25.4%; Pred. No. 0.0055;

Matches 60; Conservative 30; Mismatches 69; Indels 77; Gaps 17;

QY 28 LSVSYL--PIPE---VOCFVFNVEYMCNTMNSSE-PPPTNLTLYWYKNSDNDKVK 79

DB 17 LSVSLNQSPPEPKRYLKCSPKKEFTTCWMEPGADGCLPTNTLYT-HKEGET-LIHE 74

QY 80 CSHYLFSEETSG--COLQKKEIHLVOTFYVQLO-----QDPR-----EPRR 118

DB 75 CPDYK-----TGNPNSCYFSKHTSINKMYITVNAINQGISSDPLVYHVTYIPEP 129

QY 119 QATOMLKLQN-----LVIPAPENLILHKLSSQLELMMNRFNLHCHLEHLVQYR--- 168

DB 130 PANLTLLELKHEDRKPYLIMKWSPPPTW-----DVKSGM-----FTIOYEIRL 172

QY 169 -----TDMDSMTQESVDYRHKFSLPSVDCOKRTYTFVRSRPNLCGSAOHSEMS 219

DB 173 KPEKATWETHFTLKQQLK-IFNL--YPOCK---YLVOIRKCPDNG--YNSEMS 219

Search completed: June 28, 2002, 07:43:19

Job time: 154 sec

Fri Jun 28 07:58:58 2002

us-09-825-561a-4.rsp

Page 13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 65.65 Seconds
(without alignments)
339.569 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTILTPNGNEDTADFL.....QHWSHWSHPIHMGSNSTSKEN 232

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	369	2 A42565	interleukin-2 rece
2	1097	85.2	373	2 A55718	interleukin-2 rece
3	853.5	66.3	369	2 I49280	interleukin-2 rece
4	168.5	13.1	426	2 JC7773	IL-13alpha 1 prot
5	159	12.3	897	1 A39255	cytokine receptor
6	150	11.6	831	2 U01655	prolactin receptor
7	146.5	11.4	400	2 S06945	granulocyte-macrop
8	145.5	11.3	333	2 S13684	granulocyte-macrop
9	136.5	10.6	896	2 I56563	interleukin-3 rece
10	135.5	10.5	378	2 S50040	granulocyte-macrop
11	132.5	10.3	830	2 I50455	prolactin receptor
12	132	10.2	810	1 A33380	interleukin-4 rece
13	125	9.7	896	1 A35782	cytokine receptor
14	121.5	9.4	581	2 I45971	prolactin receptor
15	119.5	9.3	800	1 S13575	interleukin-4 rece
16	118	9.2	415	2 S12357	interleukin-5 rece
17	116	9.0	878	1 A40091	interleukin-3 rece
18	114	8.9	440	2 JI0144	interleukin-6 rece
19	114	8.9	460	2 JI0145	interleukin-6 rece
20	113	8.8	420	2 S21052	interleukin-5 rece
21	112	8.7	918	2 A36337	membrane glycoprot
22	110.5	8.6	359	2 UC7280	cytokine receptor
23	110.5	8.6	551	2 A30342	interleukin-2 rece
24	109.5	8.5	292	2 I77525	prolactin receptor
25	109.5	8.5	303	2 I77524	prolactin receptor
26	109.5	8.5	608	2 I53269	prolactin receptor
27	108.5	8.4	310	2 A29884	prolactin receptor
28	108.5	8.4	412	2 A41070	prolactin receptor
29	108.5	8.4	610	2 A34631	lactogen receptor

30	108.5	8.4	610	2 A36116	prolactin receptor
31	107	8.3	335	2 A40267	interleukin-5 rece
32	105	8.2	539	2 A35052	interleukin-2 rece
33	104.5	8.1	286	2 S50039	granulocyte-macrop
34	104.5	8.1	917	2 I49699	glycoprotein 130 -
35	98.5	7.6	918	2 A44257	interleukin-6 sign
36	97.5	7.6	608	2 S32823	somatotropin recep
37	97.5	7.6	825	1 A60386	interleukin-4 rece
38	96.5	7.5	625	2 S35317	hematopoietic grow
39	96.5	7.5	626	2 S37622	proto-oncogene - m
40	95.5	7.4	288	2 B59405	prolactin receptor
41	95.5	7.4	376	2 A59405	prolactin receptor
42	95.5	7.4	622	2 A40144	prolactin receptor
43	95.5	7.4	630	2 I51086	prolactin receptor
44	94.5	7.3	26926	2 I38344	lactin, cardiac mus
45	94	7.3	537	2 B46535	interleukin 2 rece

ALIGNMENTS

```

RESULT
1
A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A42565; A46591; I54332
R:Rakeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; M01D:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <RES>
A:Cross-references: GB:112183; NID:9307056; PIDN:AAA59145.1; PID:9219890
A:Experimental source: MOLT beta lymphoid cells
A>Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; M01D:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:112183; NID:9307056; PIDN:AAA59145.1; PID:9307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.;
Hum Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11
A:Reference number: I54332; M01D:94004847
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:119546; NID:9349631; PIDN:AC37524.1; PID:9349632
C:Genetics:
A:Gene: GDB:112RG; SCIDX1; IMD4
A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Inserts: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A>Note: defects are associated with an X-linked form of severe combined immunodeficie
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

```

Query Match 100.0%; Score 1288; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 8.8e+100;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNTILTPNGNEDTADFLITTPDLSYSTLPDEVCVFANNEYMCTNWSSEPO 60
 DB 23 LNTILTPNGNEDTADFLITTPDLSYSTLPDEVCVFANNEYMCTNWSSEPO 82


```
A>Title: Expression cloning of a receptor for human granulocyte-macrophage colony-stimulating factor  
A.Reference number: S06944; MUID:90059966
```

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A:Accession: S06945  
A:Molecule type: mRNA  
A.Residues: 1-400 <GEN>  
A:Cross-references: EMBL:X17648; NID:g32087; PIDN:CAA3638.1; PID:g32089  
R.Crosier, K.E.; Wong, G.G.; Mathey-Prevot, B.; Nathan, D.G.; Steff, C.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991  
A.Title: A functional isoform of the human granulocyte/macrophage colony-stimulating factor  
A.Reference number: A41286; MUID:91352086  
A:Accession: A41286  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A.Residues: 347-400 <CRO>  
R.Rappold, G., Willson, T.A.: Henke, A.; Gough, N.M.  
Genomics 14, 455-461, 1992  
A>Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2RA  
A.Reference number: A44474; MUID:93052350  
A:Accession: A44474  
Status: preliminary; not compared with conceptual translation  
Molecule type: DNA  
A.Residues: 7'..377-400 <RAP>  
A:CROSS-references: GB:S48539; NID:g258058; PIDD:AAB23942.1; PID:g258859  
A.Note: Sequence extracted from NCBI database (NCBIF:117980)
```

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C:Gene: GDB:GSE2RA; CSF2R  
A:CROSS-references: GDB:I18777; OMIM:306250; OMIM:425000  
A.Map position: Xp22.32-Xp22.32; YP11.3-YP11.3  
C.Keywords: glycoprotein; growth factor receptor; transmembrane protein  
F.1-32/Domain: signal sequence #status predicted <SIG>  
F.23-40/Product: granulocyte-macrophage colony stimulating factor receptor #status predicted <TM>  
F.346-346/Domain: transmembrane #status predicted <TM>  
F.446,54,59,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent) #
```

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Query Match          11.4%; Score 146.5; DB 2; Length 400;  
Best local similarity 21.1%; Pred. No. 0.00011;  
Matches    52; Conservative   44; Mismatches    90; Indels     61; Gaps      10;
```

```
OY  5 ILTPN-GNEDTTADFLTTPTSLSVSTLLPLREVOCEVFVFNVEYNCTWNSSEPQNTL 63  
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db   109 LLYPNSGRGCGTAQN-----SCFYLNADLMNCNW--ARGPTRAPDR 148  
  
OY  64 TLHWYKKSNDKNQVKCSHYLFSEEITGGCOLQ----KEFIHLXCFV 107  
       :||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db   149 QYEILTRNSKRREIRCPYLTDGSTHVGCHLDNLGLTSRNRYLVNGTSRIIGI--OFF 206  
  
OY  108 VOLDDPRE---PRQAOTMLKLONLVIYPARENILTTHKS--ESOLEMNWNFEELNHLC 160  
       :||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db   207 DSLDLTKKERFPNSVTVCRTHTCLVRW-KQRITYOKLSYLDFOQLDVRHKNKPPRG 265  
  
OY  161 LEHLVOLKYRTDMDSHEOSVDYRKFKSLPSVDGCKRRYFRVASRPRLCGSKQHRSMSH 220  
       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db   266 TENLL-----INVSGDLENRYNPSSPEPKAKHSVKIKAAADVRL---NMWSWE 311  
  
OY  221 PIHMGSN 227  
       |::|:  
Db   312 ALTFGSD 318
```

```
RESULT      8  
S13684  
granulocyte-macrophage colony-stimulating factor receptor - human  
C.Species: Homo sapiens (man)  
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999  
C.Accession: S13684; A40989  
R.Asanmorth, A.; Kraft, A.  
Nucleic Acids Res. 18, 7178, 1990  
A>Title: Cloning of a potentially soluble receptor for human GM-CSF.  
A.Reference number: S13684; MUID:91088339  
A:Accession: S13684  
A.Status: preliminary; translation not shown  
A:Molecule type: mRNA
```

A:Residues: 1-333 <ASB>
A:Cross-references: EMBL:X54935; NID:g31860; PIRN:CAA38697.1; PID:g31861
R.Raines, M.A., Liu, L.; Qian, S.G.; Joe, V.; DiPersio, J.F.; Golde, D.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 8203-8207, 1991
A>Title: Identification and molecular cloning of a soluble human granulocyte-macrophage
A.Reference number: AA0989; MUID:91376112
A.Accession: AA0989
A:Molecule type: mRNA
A:Residues: 314-333 <RAI>
A:Cross-references: GB:M73832

Query Match 11.3%; Score 145.5; DB 2; Length 333;
Best Local Similarity 21.1%; Pred. No. 0.0001;
Matches 52; Conservative 43; Mismatches 90; Indels 61; Gaps 10;

OY 5 ILTPN-GNEDTTADFLTLPTDSLSTLPRLPQCVFVFNVEYNCTMNSSSEPOPNL 63
 :|||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 109 ILYPPSGRGRTAAQN-----SCFIYNADMNCITW--ARGPRAPRDV 148

OY 64 TLHYMKNSDNDKVKCASHYLFESETISGCOLQ-----KKELHLYQTFFV 107
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 149 QTFYIKRSKRRETRCPYIIDDSGTNYGHCHDNLSGLSRMYFLVNTSREIG--QGF 206
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
OY 108 VOLODPRE----PRROATMLKLQNLVIWPARENLLHKLS--ESQLMNKNREFLNHC 160
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 207 DSLILTKTEREPSPSNVTFRCNTTHCLVRW-KOPRYOKLSYLDFOYLQVHRKNTORG 265

OY 161 LEHLIVQRDMHSMTEDSVDRHKFSIPSYOGCKRYTEFYRVSRNPICGSAGHEMSH 220
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 266 TENLL-----INVSGLDENRNFPSSRPRAKSKVITRADVRIIL---NWSSNSE 311

OY 221 PRHWGS 226
 :|||
DB 312 AIEFGS 317

RESULT 9
156563 Interleukin-3 receptor beta-subunit - rat
C.Species: Rattus sp. (rat)
C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C.Accession: 156563
R.Appel, K.; Butlini, M.; Sauter, A.; Gebicke-Haefer, P.J.
J. Neurosci. 15, 5800-5809, 1995
A>Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
A.Reference number: 156563; MUID:95370942
A.Accession: 156563
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; MID:g1086954; PIRN:AAB35068.1; PID:g1086955
C:GeneInfo: C:Genetics:
A:Gene: rIL-3RBeta
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C.Keywords: cytokine receptor
F.39-235/Domains: cytokine receptor homology <CRSI>
F.253-433/Domains: cytokine receptor homology <CRS2>

Query Match 10.6%; Score 136.5; DB 2; Length 896;
Best Local Similarity 23.9%; Pred. No. 0.0019;
Matches 48; Conservative 41; Mismatches 83; Indels 29; Gaps 11;

OY 38 VOCFVFNNVCNTNNSSEPQTNLTILHYWKNSDNDKVKCASHYLFESETISG----- 92
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 251 LOCCEPDGIOLNCSMEWMTK-VTDVSVGFLEFSSSPAAGEKCSPVV--KEIQASRYTRY 307

OY 93 -COLAKKEIHLYQTFFVOLODPREPPEATOMLKONLVIPARENLLHKLSOLELIN 151
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 308 HOSLNVSDPAHAISOYTYSVK-----RLFQGKIETEFN-HIQMNPRTLNLTKNRPS-YSLH 360

OY 152 WNNR-----FLNHCLLEHLVQYFTD--MDHSKTEDSVDRHKFSIPSYDGOKRYTEFYRS 203

Db 361 WETQKMSYEPFIOHAFQ--VOYKKKLDKRWEDSKTE--NLNHAHSMDLPOLEPRTSYCARAVK 417
 Oy 204 RFPNLCGSAQHSEMSHPH 224
 Db 418 KTIPEYKGL--WSEMSNCTW 436

RESULT 10

S50040
 granulocyte-macrophage colony-stimulating factor receptor alpha-3 chain - human
 N:Alternate names: GM-CSF receptor alpha-3 chain; hematopoietic growth factor receptor
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C:Accession: S50040; S47568
 R:Hu, X.; Zuckerman, K.S.
 A:Description: Cloning and sequencing of the cDNA encoding alternative splicing variants
 A:Reference number: S50039
 A:Accession: S50040

Molecule type: mRNA
 A:Residues: 1-378 <HUX>
 A:Cross-references: EMBL:L29349; NID:q460284; PIDN:AAA60962.1; PID:q463107
 R:Hu, X.; Emanuel, P.D.; Zuckerman, K.S.
 Biochim. Biophys. Acta 1223, 306-308, 1994
 A:Title: Cloning and sequencing of the cDNAs encoding two alternative splicing-derived
 A:Reference number: S47567; MUID:94368898
 A:Accession: S47568
 A:Molecule type: mRNA
 A:Residues: 241-315, 317-378 <HUX>
 A:Cross-references: EMBL:L29349
 C:Genetics:
 A:Gene: GM-CSF-RA3; CSF3RA
 A:introns: 316/3
 C:Keywords: alternative splicing; glycoprotein; growth factor receptor; transmembrane pr

Query Match 10.5%; Score 135.5; DB 2; Length 378;
 Best Local Similarity 20.5%; Pred. No. 0.00082;
 Matches 50; Conservative 43; Mismatches 90; Indels 61; Gaps 10;

Oy 5 ILTPN-GNETTADFLTPMTDLSVSLPLPEVQCFVFNENYMNCTNSSEPOPTNL 63
 Db 109 LTPNSRGESTAAQNF-----SCFLYNADLMCTV--AGPAPAPRV 148
 Oy 64 TLHYWYKNSDNDKVKOKSHYLFSEITSGCOLQ-----KKEIHLYQFV 107
 Db 149 QYFLYIRNSKRREINCPYIYDQSGTHVGHCHDNLGSLSRNYFLVNGTSREIGT--QPF 206
 Oy 108 VOADPRE-----PRCAOTOMLKLQMLVTPAPENILTLKLS--ESQLELNNNNRFLNHC 160
 Db 207 DSLIDTRKIERPNPNSVNYRCNTTTCGLVW-KQPTTYQKLSLTDQYOLDVHRKNTOPG 265
 Oy 161 LEHLVQRTMDHSWTEQSVDYRHKFSLPSVDQKRYTFRVRSREPLCGSAQHSEMSH 220
 Db 266 TENL-----INVSGLDENRYNFPSSPRRAKHSKIRADVRIL-----NMSSMSE 311
 Oy 221 PIHW 224
 Db 312 AIEF 315

RESULT 11

I50455
 prolactin receptor - pigeon
 C:Species: Columba livia (domestic pigeon)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
 C:Accession: I50455
 R:Chen, X.; Horsman, N.D.
 Endocrinology 135, 269-276, 1994
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
 A:Reference number: I50455; MUID:94283267
 A:Accession: I50455

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:q466381; PIDN:AAA20646.1; PID:q466382
 C:Superfamily: cytokine receptor homology
 F:36-220/Domain: cytokine receptor homology <CRS1>
 F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match

10.3%; Score 132.5; DB 2; Length 830;
 Best Local Similarity 22.2%; Pred. No. 0.0038;
 Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;

Oy 38 VQCFVNEVEMNCTWNSSE-POPTNLTLHYTKNSDNDKVKOKSHYLFSEITSGCOLQ 96
 Db 34 IRCRSLEKETFSQWKKPGSDGGLPTNYTL--FYSKDSERKIECPDYGMSG--PNSCYED 89
 Oy 97 KKEIHLYQFVVOADPREPRQAT--QMLKLQNLVTPAPENILTLH--KLSEOLELN 151
 Db 90 KNHTNPMTTITNYMANNEIGSNSDQYVDYTSIQPDPAPVLSLETTSASTTYLLAK 149
 Oy 152 WNNRFL-----NHCEHLVQRTMDHSWTEQSVDYRHKFSLPSVDGQKRYTFRYSRE 205
 Db 150 WSPPLADVTSNSHYRYELRLKPEKEKEWETVSGVQTKVNRLOAGVKYVQRCVL 209
 Oy 206 NPLCGSAQHSEMSHPH 223
 Db 210 D-----IGEMSEMSERN 222

RESULT 12

A33380
 interleukin-4 receptor precursor - mouse

N:Alternate names: IL-4 receptor
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 01-Dec-2000
 C:Accession: A33380; B33380; C33380; A34861; I54232
 R:Moisley, B.; Beckmann, M.P.; March, C.J.; Idzerda, R.L.; Gimpel, S.D.; Vandenbos, T.
 Widmer, M.B.; Cosman, D.; Park, L.S.
 Cell 59, 335-348, 1989
 A:Title: The murine interleukin-4 receptor: molecular cloning and characterization of
 A:Reference number: A90911; MUID:90030408

A:Accession: A33380
 A:Molecule type: mRNA
 A:Residues: 1-810 <MO1>
 A:Cross-references: GB:M27959; NID:q198363; PIDN:AAA39299.1; PID:q309408
 A:Accession: B33380
 A:Molecule type: mRNA
 A:Residues: 1-258 <MO2>
 A:Accession: C33380
 A:Molecule type: mRNA
 A:Residues: 1-224, 'PSNENL' <MO3>
 A:Cross-references: GB:M27960; NID:q198365; PIDN:AAA39300.1; PID:q309409
 A:Note: three forms of cDNA were isolated; the amino end of the mature protein, was con
 acellular domain and may encode a soluble form of the receptor
 R:Harada, N.; Castle, B.E.; Cosman, D.M.; Itoh, N.; Schreurs, J.; Barrett, R.L.; Howa
 Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
 A:Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor base
 A:Reference number: A34861; MUID:90138976
 A:Accession: A34861
 A:Molecule type: mRNA
 A:Residues: 1-810 <HAR>

A:Cross-references: GB:M29854; NID:q198346; PIDN:AAA39297.1; PID:q309407
 R:Wrighton, N.C.; Campbell, L.A.; Lee, F.D.
 Growth Factors 6, 103-118, 1992
 A:Title: The murine interleukin-4 receptor gene: Genomic structure, expression and po
 A:Reference number: I54232; MUID:92265335
 A:Accession: I54232
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-73, 'T', 75-333, 'P', 335-810 <RES>
 A:Cross-references: GB:M64879; NID:q198359; PIDN:AA859727.1; PID:q198361

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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 43.94 Seconds
(without alignments)
128.965 Million cell updates/sec

Title: US-09-825-561a-4
Perfect score: 1288
Sequence: 1 LMTTILTPNGNEDTADPFL.....QHMSEMSPIHMGNTSKEN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

tal number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1288	100.0	347	1 US-08-052-205-7	Sequence 7, Appli
2	1288	100.0	347	1 US-08-595-974-7	Sequence 7, Appli
3	1288	100.0	369	1 US-08-052-205-4	Sequence 4, Appli
4	1288	100.0	369	1 US-08-595-974-4	Sequence 4, Appli
5	1277	99.1	230	1 US-08-052-205-11	Sequence 11, Appli
6	1277	99.1	230	1 US-08-595-974-11	Sequence 11, Appli
7	1277	99.1	252	1 US-08-052-205-9	Sequence 9, Appli
8	1277	99.1	252	1 US-08-595-974-9	Sequence 9, Appli
9	853.5	66.3	369	2 US-08-424-224-2	Sequence 2, Appli
10	853.5	66.3	369	5 PCT-US94-02891-69	Sequence 2, Appli
11	207	16.1	380	1 US-08-609-572-4	Sequence 4, Appli
12	207	16.1	380	1 US-08-841-751-4	Sequence 4, Appli
13	207	16.1	380	4 US-08-846-340-4	Sequence 4, Appli
14	207	16.1	380	4 US-08-846-344-4	Sequence 4, Appli
15	199.5	15.5	383	4 US-08-609-572-2	Sequence 2, Appli
16	199.5	15.5	383	4 US-08-841-751-2	Sequence 2, Appli
17	199.5	15.5	383	4 US-08-846-340-2	Sequence 2, Appli
18	199.5	15.5	383	4 US-08-846-344-2	Sequence 2, Appli
19	178	13.8	427	4 US-08-969-125-9	Sequence 9, Appli
20	159	12.3	897	1 US-07-960-389-2	Sequence 2, Appli
21	150.5	11.7	552	1 US-08-243-010-6	Sequence 6, Appli
22	146.5	11.4	400	1 US-08-351-149-6	Sequence 6, Appli
23	146.5	11.4	400	1 US-08-384-828-6	Sequence 6, Appli
24	146.5	11.4	400	1 US-08-895-474-6	Sequence 6, Appli
25	126	9.8	606	4 US-09-523-217-97	Sequence 97, Appli
26	120	9.3	538	3 US-09-040-005-2	Sequence 2, Appli
27	120	9.3	538	4 US-09-522-217-115	Sequence 115, App

28	118	9.2	335	1 US-07-947-130-3	Sequence 3, Appli
29	118	9.2	335	1 US-08-421-822-3	Sequence 3, Appli
30	118	9.2	335	1 US-08-421-823-3	Sequence 3, Appli
31	118	9.2	398	1 US-07-757-390-6	Sequence 6, Appli
32	118	9.2	398	1 US-08-442-282-6	Sequence 6, Appli
33	118	9.2	398	1 US-08-442-281-6	Sequence 6, Appli
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35	118	9.2	415	1 US-07-757-390-5	Sequence 5, Appli
36	118	9.2	415	1 US-08-442-282-5	Sequence 5, Appli
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39	115	8.9	315	1 US-07-757-390-8	Sequence 8, Appli
40	115	8.9	315	1 US-08-442-282-8	Sequence 8, Appli
41	115	8.9	315	1 US-08-442-281-8	Sequence 8, Appli
42	115	8.9	315	2 US-08-939-727-8	Sequence 8, Appli
43	115	8.9	332	1 US-07-757-390-7	Sequence 7, Appli
44	115	8.9	332	1 US-08-442-282-7	Sequence 7, Appli
45	115	8.9	332	1 US-08-442-281-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-052-205-7
; Sequence 7, Application US/08052205
; Patent No. 5510259
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHTA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,205
; FILING DATE: 19930422
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5510259man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-052-205-7

Query Match 100.0%; Score 1288; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 9,5e-119;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTILPFGNEDTADFFLTPTDLSVSTLPPEVQCFVFNVEYMNCTMNSSSEPOP 60
DB 1 LNTILPFGNEDTADFFLTPTDLSVSTLPPEVQCFVFNVEYMNCTMNSSSEPOP 60

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120
DB 61 TNLTLHWYKNSDNDKVKQCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120

QY 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTFYVOLDDPREPRROA 180
DB 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTFYVOLDDPREPRROA 180

QY 181 DYRHKFSLPSVDGQKRYTFVRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSKEN 232
DB 181 DYRHKFSLPSVDGQKRYTFVRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSKEN 232

RESULT 2
US-08-595-974-7
Sequence 7, Application US/08595974
Patent No. 5705608
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-7

Query Match 100.0%; Score 1288; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 9,5e-119;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LNTILPFGNEDTADFFLTPTDLSVSTLPPEVQCFVFNVEYMNCTMNSSSEPOP 60

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120
DB 61 TNLTLHWYKNSDNDKVKQCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120

QY 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTFYVOLDDPREPRROA 180
DB 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTFYVOLDDPREPRROA 180

QY 181 DYRHKFSLPSVDGQKRYTFVRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSKEN 232
DB 181 DYRHKFSLPSVDGQKRYTFVRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSKEN 232

RESULT 3
US-08-052-205-4
Sequence 4, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-052-205-4

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Best Local Similarity	100.0%	Pred. No. 1e-118		
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Db	23	LNTLTLPNGEDTTADFLTTPMTSLSVSTLPRLPEVQCEFVENYEMNCNTSSSEDP	82	
QY	61	TNLTLTHTYKNSDNDKVKCSHYLPSEETSGCOLKKEIHHYQFVYVLODPRPRKQA	120	
Db	83	TNLTLTHTYKNSDNDKVKCSHYLPSEETSGCOLKKEIHHYQFVYVLODPRPRKQA	142	
QY	121	TQMCLKQMLVTPMARENLTTLKLSQLELWMNNRFLNHCLEHLYQYRTDMDSHTESQY	180	
Db	143	TQMCLKQMLVTPMARENLTTLKLSQLELWMNNRFLNHCLEHLYQYRTDMDSHTESQY	202	
QY	181	DYRHKFSLPVSDGQKRYFRVRSRNPYLCGSAQHSSEMSHPRHMSNSTKEN	232	
Db	203	DYRHKFSLPVSDGQKRYFRVRSRNPYLCGSAQHSSEMSHPRHMSNSTKEN	254	

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1      RESULT      4
2      US-08-595-974-4
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4      : Patent No. 5705608
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: SUGAMURA, KAZUO
8      : APPLICANT: TAKESHITA, TOSHIKAZU
9      : APPLICANT: ASAO, HIRONOBU
10     : APPLICANT: NAKAMURA, MASATKA
11     : APPLICANT: SHIMAMURA, TOSHIRO
12     : APPLICANT: SUZUKI, MANABU
13     : APPLICANT: HAMURO, JUNJI
14     : TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
15     : NUMBER OF SEQUENCES: 21
16     :
17     : CORRESPONDENCE ADDRESS:
18     :
19     : ADDRESSEE: OBLO, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,
20     : ADDRESSEE: P.C.
21     : STREET: 1755 S.
22     : CITY: Arlington
23     : STATE: Virginia
24     : COUNTRY: U.S.A.
25     :
26     : ZIP: 22202
27     :
28     : COMPUTER READABLE FORM:
29     : MEDIUM TYPE: Floppy disk
30     : COMPUTER: IBM PC compatible
31     : OPERATING SYSTEM: PC-DOS/MS-DOS
32     : SOFTWARE: Patentin Release #1.0, Version #1.25
33     :
34     : CURRENT APPLICATION DATA:
35     : APPLICATION NUMBER: US/08/595,974
36     : FILING DATE: 06-FEB-1996
37     :
38     : CLASSIFICATION: 435
39     :
40     : PRIOR APPLICATION DATA:
41     : APPLICATION NUMBER: US 08/052,205
42     : FILING DATE: 22-APR-1993
43     : APPLICATION NUMBER: JP 104947/1992
44     : FILING DATE: 23-APR-1992
45     :
46     : ATTORNEY/AGENT INFORMATION:
47     : NAME: OBLO, No. 5705608man F.
48     : REGISTRATION NUMBER: 24,618
49     : REFERENCE/DOCKET NUMBER: 10-615-0X
50     : TELECOMMUNICATION INFORMATION:
51     : TELEPHONE: (703) 413-3000
52     : TELEFAX: (703) 413-2220
53     :
54     : TELEX: 248855 OPAT UR
55     : INFORMATION FOR SEQ ID NO: 4:
56     : SEQUENCE CHARACTERISTICS:
57     : LENGTH: 369 amino acids
58     : TYPE: amino acid
59     : TOPOLOGY: linear
60     :
61     : MOLECULE TYPE: protein
62     :
63     : US-08-595-974-4

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Query Match	100.0%;	Score 1288;	DB 1;	Length 369;
Best Local Similarity	100.0%;	Pred. No. 1e-118;		
Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	23	LNTTILTPNGENETTDADFELTTPMPDLSUSVTLPLPEVQCVFVNEVYMNCTWNSSSEPOP	82	
QY	61	TNTLTHWYNSNDKAVQCSHYLFSEETSSCQLOKKEIHLVOTFVVOLODPEPEPRA	120	
Db	83	TNTLTHWYNSNDKAVQCSHYLFSEETSSCQLOKKEIHLVOTFVVOLODPEPEPRA	142	
QY	121	TQMILQNLNVIWPAPENLTLHKLSQSLELNMNNFHLHCEHLVQYRTDMDHSWTESQV	180	
Db	143	TQMILQNLNVIWPAPENLTLHKLSQSLELNMNNFHLHCEHLVQYRTDMDHSWTESQV	202	
QY	181	DYRKHFSLPEVVDGOKRYTFPRVSRFPPLCGSAQMSHSESHIIMGSMSTKEN	232	
Db	203	DYRKHFSLPEVVDGOKRYTFPRVSRFPPLCGSAQMSHSESHIIMGSMSTKEN	254	

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RESULT      5
US-08-052-205-11
? Sequence 11, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
APPLICANT: SUGAMODA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No., 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-052-205-11

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Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 6,4e-118; Mismatches 0; Indels 0; Gaps 0;
Matches 230; Conservative 0;

QY 1 LNTTILPNGNEDTADFFLTTPMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
DB 1 LNTTILPNGNEDTADFFLTTPMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
QY 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
DB 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
QY 121 TOMLKQNLVTPMAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
DB 121 TOMLKQNLVTPMAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
QY 181 DYRHKFSLPSVDGQKRYTFVRVRSRPNPLCGSAQHSWSESHPIHWSNTSK 230
181 DYRHKFSLPSVDGQKRYTFVRVRSRPNPLCGSAQHSWSESHPIHWSNTSK 230

RESULT 6
US-08-595-974-11
Sequence 11, Application US/08595974
Patent No. 5705608
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-11

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 6,4e-118; Mismatches 0; Indels 0; Gaps 0;
Matches 230; Conservative 0;

QY 1 LNTTILPNGNEDTADFFLTTPMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
DB 1 LNTTILPNGNEDTADFFLTTPMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
QY 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
DB 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
QY 121 TOMLKQNLVTPMAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
DB 121 TOMLKQNLVTPMAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
QY 181 DYRHKFSLPSVDGQKRYTFVRVRSRPNPLCGSAQHSWSESHPIHWSNTSK 230
181 DYRHKFSLPSVDGQKRYTFVRVRSRPNPLCGSAQHSWSESHPIHWSNTSK 230

RESULT 7
US-08-052-205-9
Sequence 9, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-052-205-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 7.3e-118;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LNTTITPANGNDTADAFITMTPTDLSYSTPLPEVOCFVFNVEVMNCTWNSSEPOP 60
DB 23 LNTTITPANGNDTADAFITMTPTDLSYSTPLPEVOCFVFNVEVMNCTWNSSEPOP 82
QY 61 TNLTLHWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEHLVOTFVVOLODPRERRQA 120
DB 83 TNLTLHWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEHLVOTFVVOLODPRERRQA 142
QY 121 TQMLKQNLVITPAPENLTLHKLSQLELMNNRFLNHCHLEHLVQYRTDMDHSMTEQSV 180
DB 143 TQMLKQNLVITPAPENLTLHKLSQLELMNNRFLNHCHLEHLVQYRTDMDHSMTEQSV 202
QY 181 DYRRKESLSVDGQKRYTFRVRSRFPICGSAOHMSEKSHPIHWSNTSK 230
DB 203 DYRRKESLSVDGQKRYTFRVRSRFPICGSAOHMSEKSHPIHWSNTSK 252
  
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RESULT 8

US-08-595-974-9
 ; Sequence 9, Application US/08595974
 ; Patent No. 5705608

GENERAL INFORMATION:

APPLICANT: SUGAMURA, KAZUO
 APPLICANT: TAKESHITA, TOSHIKAZU
 APPLICANT: ASAO, HIROMOBU
 APPLICANT: NAKAMURA, MASATAKA
 APPLICANT: SHIMAMURA, TOSHIRO
 APPLICANT: SUZUKI, MANABU
 TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/595,974
 FILING DATE: 06-FEB-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,205
 FILING DATE: 22-APR-1993
 APPLICATION NUMBER: JP 104947/1992
 FILING DATE: 23-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5705608man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 10-615-0X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 252 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-595-974-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 7.3e-118;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LNTTITPANGNDTADAFITMTPTDLSYSTPLPEVOCFVFNVEVMNCTWNSSEPOP 60
DB 23 LNTTITPANGNDTADAFITMTPTDLSYSTPLPEVOCFVFNVEVMNCTWNSSEPOP 82
QY 61 TNLTLHWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEHLVOTFVVOLODPRERRQA 120
DB 83 TNLTLHWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEHLVOTFVVOLODPRERRQA 142
QY 121 TQMLKQNLVITPAPENLTLHKLSQLELMNNRFLNHCHLEHLVQYRTDMDHSMTEQSV 180
DB 143 TQMLKQNLVITPAPENLTLHKLSQLELMNNRFLNHCHLEHLVQYRTDMDHSMTEQSV 202
QY 181 DYRRKESLSVDGQKRYTFRVRSRFPICGSAOHMSEKSHPIHWSNTSK 230
DB 203 DYRRKESLSVDGQKRYTFRVRSRFPICGSAOHMSEKSHPIHWSNTSK 252
  
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RESULT 9

US-08-424-224-2
 ; Sequence 2, Application US/08424224
 ; Patent No. 5912173

GENERAL INFORMATION:

APPLICANT: LEONARD, WARREN J.
 TITLE OF INVENTION: MURINE IL-2R CDNA AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVE.
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT # 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,224
 FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/121,435
 FILING DATE: 14-SEPT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WILLIAM S. FELLER
 REGISTRATION NUMBER: 26,728
 REFERENCE/DOCKET NUMBER: 2026-4061051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-4800
 TELEFAX: 212-751-6849
 TELEEX: 421792
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 369
 TYPE: AMINO ACID
 TOPOLOGY: UNKNOWN

MOLECULE TYPE:

DESCRIPTION: PROTEIN
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: MURINE
 INDIVIDUAL ISOLATE: IL-2R
 US-08-424-224-2


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Oy 9 NGNETTADDFLTJMPPTDSLSVSTLPLPEYOCFVENFENYCNMCNNSSEDP-----T 61
    || : : : ||
Db 115 NGSE VOSSMAETTYWISPOCIPETKYQDDMCYVYNNQTHLCSW-----KPGIYLDT 167
    || : : : ||

Oy 62 NLTLTHYWRKNSDNDRVOKCSHYLFSEETISGCOLKKEHLVOTFYVOLDPRE--PRQ 119
    || : : : || : : : || : : : ||
Db 168 NYNLFWEYEGDHD--ALQCVQYIKADQNGICRRPYLEADYKDFYICVANGSENKPIRS 225
    || : : : || : : : || : : : ||

Oy 120 ATOMLKIONLVIIPAENLTLHKLSQBLENNN---NRFNLHCLEHLVORTDDHSHWT 176
    || : : : || : : : || : : : || : : : ||
Db 226 SYTFEOLONIKPRLPYLFTFRSESCSEIKLWISPLGPJPACFDYEIRED-DTTLV 284
    || : : : || : : : || : : : || : : : ||

Oy 177 EQSDVRRKRELSVDDQGRKTFEVRGRPNPLGSAQHSWMSHPHM--CSNJSKE 231
    || : : : || : : : || : : : || : : : ||
Db 285 TAYVE-NETTLTKTNETRQLCFVVRKRVNINYCDDGCIWSEMSDKOCWSEEDSLK 339
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1      RESULT 12
2      US-08-841-751-4
3      Sequence 4, Application US/08841751
4      Patent No. 6214559
5      GENERAL INFORMATION:
6      APPLICANT: Collins, Mary
7      APPLICANT: Donaldson, Debora
8      APPLICANT: Fitz, Lori
9      APPLICANT: Neben, Tamlyn
10     APPLICANT: Whilters, Matthew
11     APPLICANT: Wood, Clyde
12     TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
13     NUMBER OF SEQUENCES: 9
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Genetics Institute, Inc.
16     STREET: 87 Cambridgepark Drive
17     CITY: Cambridge
18     STATE: MA
19     COUNTRY: USA
20     ZIP: 02140
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: Patent Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/08/841,751
28     FILING DATE:
29     CLASSIFICATION:
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: 08/609,572
32     FILING DATE:
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Brown, Scott A.
35     REGISTRATION NUMBER: 32,724
36     REFERENCE/DOCKET NUMBER: G15268
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: (617) 498-8224
39     TELEFAX: (617) 876-5851
40     INFORMATION FOR SEQ ID NO: 4:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 380 amino acids
43     TYPE: amino acid
44     TOPOLOGY: linear
45     MOLECULE TYPE: protein
46     US-08-841-751-4

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	Query Match	16.1%	Score 207;	DB 4;	Length 380;	
	Best Local Similarity	25.4%;	Pred. No. 1,9e-12;			
	Matches	60;	Conservative 46;	Mismatches 106;	Indels 24;	Gaps 9;
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Db	115	NGSE-VOSSMAETWISPGIGPETKRVDDMDCVYYNMWGLICSW-----RKGIQLVDLT	167			

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Oy      62 NLTLLHWKNSNDKQKQKCSHYLSEETSSCOLOKKEHILHYQFVVOLODPRE--PRQ 119
      168 NNNLEWYEGDHH--ALCQCVYIADGONIGCRPYLEASDYKPFYICVNGSSENKPIRS 225
Oy      120 ATQMLKLONLVTPAPENULTLHKISEQLELNWV---NRFNLHCLHLYQRTIDHDSWT 176
      226 STEFFQLONIYKPLRPVYLITRRESSCIRKIKWSIPLGPIPARCEYDEIETRED--DTLLV 284
Db      177 EOSVDYRHRKFSIPSDVGOKRYTFRYRSRFPNPLCSAOWMSWSPHFW-GSNTSKE 231
      285 TAYVE-NETTYLTKTTNETRQLCFVYRSKVNIIYCSDDGIGWSWSKQSCQWEGEDLSKK 339

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13
US-08-846-340-4
Sequence 4, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debora
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

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[illegible]

,Fri, Jun 28 07:58:57 2002

us-09-825-561a-4.ra1

Page 9

Job time: 54 sec

4

5

6

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 63.41 Seconds
(without alignments)
632.942 Million cell updates/sec

Title: US-09-825-561a-4
Perfect score: 1288
Sequence: 1 LNTTILTPNGNEDTTADFFL.....QHWSESHPIHWSNTSKEN 232

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	Length	DB ID	Description
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2	259.5	20.1	404	13	Q90X88	Q90X88 oncorhynchu
3	213	16.5	386	6	Q95LF0	Q95LF0 canis famli
4	199.5	15.5	383	11	Q88786	Q88786 mus musculu
5	178	13.8	427	4	Q96B84	Q96B84 homo sapien
6	172.5	13.4	405	6	Q95LE1	Q95LE1 canis famli
7	159.5	12.4	371	4	Q9HC73	Q9HC73 homo sapien
8	141.5	11.0	279	4	Q9UDY5	Q9UDY5 homo sapien
9	139	10.8	890	11	Q9Z1A0	Q9Z1A0 cavia porce
10	137.5	10.7	415	11	Q9Z0K4	Q9Z0K4 cavia porce
11	137.5	10.7	881	13	Q95J19	Q95J19 xenopus lae
12	137	10.6	349	6	Q97597	Q97597 bos taurus
13	136.5	10.6	896	11	Q64146	Q64146 rattus norv
14	136	10.6	232	4	Q9H5R3	Q9H5R3 homo sapien
15	130	10.1	611	13	Q91BFG	Q91BFG xenopus lae
16	130	10.1	611	13	Q9PT10	Q9PT10 xenopus lae

17	130	10.1	810	11	Q54690	Q54690 mus musculu
18	128	9.9	810	11	Q60583	Q60583 mus musculu
19	125	9.7	611	13	Q9PT89	Q9PT89 xenopus lae
20	124.5	9.7	918	13	Q9W6U9	Q9W6U9 gallus gall
21	121.5	9.4	296	6	Q18880	Q18880 bos taurus
22	120.5	9.4	229	11	Q91W8	Q91W8 rattus norv
23	120.5	9.4	801	11	Q91W8	Q91W8 rattus norv
24	120	9.3	538	4	Q9HBE5	Q9HBE5 homo sapien
25	120	9.3	538	4	Q9HBE5	Q9HBE5 homo sapien
26	119.5	9.3	800	11	Q63257	Q63257 rattus norv
27	118.5	9.2	370	11	Q91J07	Q91J07 mus musculu
28	117.5	9.1	359	11	Q91J07	Q91J07 mus musculu
29	116.5	9.0	359	11	Q91J07	Q91J07 mus musculu
30	115.5	9.0	359	11	Q91J07	Q91J07 mus musculu
31	115	8.9	414	11	Q920B8	Q920B8 rattus norv
32	115	8.9	414	11	Q920B8	Q920B8 rattus norv
33	113.5	8.8	626	13	Q90W67	Q90W67 cynops pyr
34	113	8.8	420	4	Q14633	Q14633 homo sapien
35	112	8.7	396	4	Q14631	Q14631 homo sapien
36	112	8.7	602	13	Q90ZB0	Q90ZB0 carassius a
37	111	8.6	625	6	Q9XS92	Q9XS92 trichosurus
38	110	8.5	425	11	Q90M58	Q90M58 mus musculu
39	110	8.5	600	13	Q9PT80	Q9PT80 carassius a
40	109.5	8.5	608	11	Q93J21	Q93J21 mus musculu
41	107	8.3	333	4	Q15469	Q15469 homo sapien
42	106.5	8.3	422	4	Q75462	Q75462 homo sapien
43	106	8.2	227	6	Q9GLW3	Q9GLW3 ursus marit
44	105	8.2	581	6	Q46561	Q46561 ovis aries
45	105.5	8.2	422	4	Q90VH5	Q90VH5 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	343 AA.
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AC	Q9DE01			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CYTOKINE RECEPTOR COMMON GAMMA CHAIN.			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostomi;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21287902; PubMed=11394690;			
RA	Wang T., Secombes C.J.;			
RT	"Cloning and expression of a putative common cytokine receptor gamma			
RT	chain gene in rainbow trout (Oncorhynchus mykiss)."			
RL	Fish and Shellfish Immunol. 11:233-244(2001).			
DR	EMBL; AJ276623; CAC09429.2; -			
KW	Receptor.			
SO	SEQUENCE	343 AA;	39486 MW;	ED8429E7534B21EB CRC64;
Query Match	22.0%;	Score 283.5;	DB 13;	Length 343;
Best Local Similarity	30.9%;	Pred. No. 3.7e-19;		
Matches	59;	Conservative 37;	Mismatches 88;	Indels 7;
			Gaps 4;	
QY	36 PEVCGFVNEVYMKCTNSSEPOPTNLTFLHWYKNSDNDKYOKSCHYFSEITSGOL 95			
DB	23 PNVCLTINDYVNCVTSSEQSIPE-VNFT--FSSSPFIDNMECTTYIQESYAVGCR 79			
QY	96 QKKRIHLVQFFVVOLODPREPRROATQMLKQNLVTPAPENLTLLKLSQSLEINMNR 155			
DB	80 SYDSDFRFLTKLV--HQNMSYQODHLKSMVXLTPVNLSTVMNDRPDLNLTWNNS 136			
QY	156 FLNCLTSLVQYRDMQHSWTEOSVDYRHKFSLPSVDGQKRTFRFRSFPNLCGSAQHW 215			

D6 137 KMTCTCESEVRIRINSD-KMKTSTPSEQKAVAFPLASSRIEFQVRRARVDMGGESEFW 195

QY 216 SEMSHPIHNGS 226
|||||
D6 196 SEMSQPIQNDSD 206

RESULT	2
900XP8	
ID	Q90XP8
AC	Q90XP8;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	INTERLEUKIN 13 RECEPTOR ALPHA-2.
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX	[1]
RN	MBL_Jaxid-8022;
NA	SEQUENCE FROM N.A.
NA	Lockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,
NA	Secombes C.J.;
RT	"Isolation and characterization of a putative interleukin 13 receptor
RT	alpha-2 sequence from rainbow trout (Oncorhynchus mykiss).",
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBO databases.
DR	EMBL; AF361437; AAL26921.1; -.
DR	Receptor.
SO	SEQUENCE
404 AA:	46728 MW; 48987E34CFEB6D6 CRC64;

[illegible]

RESULT	3		
RT	095LF0		
AC	095LF0	PRELIMINARY;	PRT; 386 AA.
DT	01-DEC-2001	(TREMBLE, 19, Created)	
DT	01-DEC-2001	(TREMBLE, 19, last sequence update)	
DT	01-DEC-2001	(TREMBLE, 19, last annotation update)	
DE	INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 2.		
GN	IL13RA2.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_Taxid=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21287533; PubMed=11389954;		
RA	Tang L.;		
RT	"Molecular cloning of canine IL-13 receptor alpha chain (alpha		
RT	alpha) cDNAs and detection of corresponding mRNAs in canine		
RT	tissues.";		

RL Vet: Immunol. Immunopathol. 79:181-195(2001).
DR EMBL; AF314533; AAL14887.1; -.
KM Receptor.
SQ SEQUENCE 386 AA; 45110 MW; A16FDF2DD023ED95 CRC64;

Query Match 16.5%; Score 213; DB 6; Length 386;
Best Local Similarity 25.8%; Pred. No. 2.4e-12;
Matches 61; Conservative 38; Mismatches 107; Indels 30; Gaps 8;

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Oy      3  TTILT--ENGEDETADPELTTPRTDLSLSVSLPLPEVOCCVFEVFEVFNCTNNSSSEPP--P  60
      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      125 TTYTSTSQCKREI-----KIQDDMDCYIYNMQLYVCSMKPMKGVHFD  160

Oy      61 TNLTLHWYKNSNDKDYKCKSHYLPSEBITSGCOLQKKEIHLVQTFEVLQADPRE--PRR  110
      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      166 TNYQLFEWYSGIDHS--ACTDYLIVNCKNNKNGCFPLESSDYKDFICVNGSSSEQPIR  220

Oy      119 QATQMLKQLNVLTPAPENLILHLKLSOLELANN---NRLNHCLEHLVQRTIDMDSW  170
      | : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      224 PSYFIQQLQIVKPMPPDYLSLTIVNKEEINILKNNMKPCGIPAKCFIYEIEFTED--GTTW  280

Oy      176 TEGSVDIRHAFSLPSYDQGRKRTTFVRVRERFPLCGSNQHMSEASHPIHNGSNINRKE  231
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      283 VTTVEVEIQLITRTSNESQK--LCFLIVSRKVNLYVCSDDGINSWSEDECKMGIDLWE  337

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RESULT	4		
ID	088786	PRELIMINARY;	PRT; 383 AA.
AC	088786;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	IL-13 RECEPTOR ALPHA 2 (INTERLEUKIN 13 RECEPTOR, ALPHA 2).		
GN	IL13RA2.		
OS	Mus musculus (Mouse).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Soturognathii; Muridae; Murinae; Mus.		
OX	Mamm_Taxid=10090;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C3H/HEJ; TISSUE=THYMUS;		
RX	MEDLINE=98391042; Pubmed=9723226;		
RA	Donaldson D.D., Whithers M.J., Fitz L., Neben T.Y., Finerly H.,		
RA	Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,		
RT	Collins M.		
RT	"The murine IL-13 receptor alpha 2: molecular cloning,		
RL	characterization, and comparison with murine IL-13 receptor alpha 1.",		
RL	J. Immunol. 161:2317-2324(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Straussberg R.;		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: U65747; AAC33240.1; "		
DR	EMBL: BC003723; AAH03723.1; "		
DR	HSSP: P16471; IBP3.		
DR	MGP: MGI:1277954; I113ra2.		
DR	InterPro: IPR002965; CR1A.		
DR	InterPro: IPR003532; Hematopo_receptor_S_F2.		
DR	PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.		
KW	Receptor.		
SO	SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;		

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Query Match      15.5%  Score 199.5; DB 11;  length 383;
Best Local Similarity 25.7%;  Pred No. 4,7e-11;
Matches 53;  Conservative 40;  Mismatches 108;  Indels 11;  Gaps
7;

QY 25 TDSLSVSTLPLEPVQCFVNEVEMNCTWN-SSSEQPTNLTLATWYKNSDNDKVVQKCSH 83
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 SDESLEFL-KIDMKCLCYIMQWLVCSSMKPCTGVSDNTNIMFPEWYGLDH--ALQCA 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 84 LSEETITSCQLOKKEIHLYQTFVVOI--QDREPRROATOMLKLONLVIWAPENITLH 141
 182 LQDEKNVCKSLNLDSSDYKDFECIVNGSSKLEPIRSSYVFOLONIYKPLPPEFLHIS 241
 QY 142 KISESLELNMN--NRFLNHGLEHLVQYRTDMDSHTQESQYDHKKSLSPVQOKRYT 198
 Db 242 VENSIDIRKMSVPGSGPIPPCTTYEIVRED-DISW-ESATDKMDKLKRRANSEDL 299
 QY 199 FVRSRPNPLCGSAOHMSHPIHNGSNTSKEN 232
 Db 300 FVFRCKVNIYCADDDGIMSESECEGEGYTPDS 333

RESULT 5
 Q96BB4 PRELIMINARY; PRT; 427 AA.
 AC Q96BB4:
 NT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE INTERLEUKIN 13 RECEPTOR, ALPHA 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBL_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON ADENOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC015768; AAL15768.1;
 KW Receptor.
 SQ SEQUENCE 427 AA; 48676 MW; E6A42F7466A39A09 CRC64;

Query Match 13.8%; Score 178; DB 4; Length 427;
 Best Local Similarity 26.7%; Pred. No. 6.2e-09;
 Matches 58; Conservative 38; Mismatches 83; Indels 38; Gaps 11;

QY 37 EVOCCFNVNEMNCNTNNSSEPOP-TNLTLHYWKNSDMKYOKSHYFSEITSGC-- 93
 Db 131 ELDCITMHNLSYKMGCSMLPGRNTSPDTNVTLYWHRSL-EKIHQCN-IFREGYFGCSF 187
 QY 94 QLOKKEIHLYQTFVVOI--QDREPRROATOMLKLONLVIWAP--ENLTLHKLSESOLE 149
 Db 188 DLKRVDSPEQSHVOIMKDNAGKIKPSFNIVPLTSVYKPPPHIKNLSPH--NDPLY 244
 150 LNMNN--RFLNHGLEHLVQYRTDMDSHTQESQYDHKKSLSPVQOKRYT 189
 Db 245 VQENPNQNFISRL--FYEVVNNQTFETHNVFYVOEAKCENDEFEFERNVENTSCFVVP 300
 QY 190 SYDQKRYTFRVRSRPNPLC-GSAOHMSHPIHNG 225
 Db 301 GVLDPDLNTVIRIVKTKKCYEDDKIMSNWQSMGIG 337

RESULT 6
 Q95LEF1 PRELIMINARY; PRT; 405 AA.
 AC Q95LEF1:
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 1 (FRAGMENT).
 GN IL13RA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NC NCBL_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21287533; PubMed=11389954;
 RA Tang L.;

RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
 RT alpha2) cDNAs and detection of corresponding mRNAs in canine
 RT tissues.";
 RT Vet. Immunol. Immunopathol. 79:181-195(2001).
 DR EMBL; AF314532; AAL14886.1;
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 405 AA; 46328 MW; 926ELAC7BE53F42 CRC64;

Query Match 13.4%; Score 172.5; DB 6; Length 405;
 Best Local Similarity 25.7%; Pred. No. 1.9e-08;
 Matches 68; Conservative 36; Mismatches 110; Indels 51; Gaps 13;

QY 1 LNTTILTPNGNEDPTADDFLTTPMPTDLSVSTLP-----LPEVQCFVNEVMNCWTW 52
 Db 68 LNERICLQVSSQCTNE--SDNPSILVEKCPPEPGDPEASVTELOQVWHLNLSYKCTW 124
 QY 53 NNSSEPOP-TNLTLHYWKNSDMKYOKSHYFSEITSGOL-----QKKEIHLYQ 104
 Db 125 LPGRNTSPDTNVTLYWHR--SSLGKILQCED-IYREGQIHGCSFALTNLKDSSFEQHSVO 181
 QY 105 TFVVOLODREPRROATOMLKLONLVIWAPENITLHKLSESOLELNMN--RFLNHGLE 162
 Db 182 ---IMVKDNARKIRPSFNIVPLTSVYKPPPHIKRLF-FQNGMLYQWKNPNQNFYSRL 236
 QY 163 HLVOYRTDMDSHTQESQYDHKKSLSPVQOKRYTFRVRSR 204
 Db 237 ---SYQEVNNSQTFETHNVFYVOEAKCQNSFEFGNLEGTICFWPGVLPDLNTVIRIVR 293
 QY 205 FNPPLC-GSAOHMSHPIHNGSNT 228
 Db 294 TNKLCYEDDKIMSNWQSMGIGENT 318

RESULT 7
 Q9HC73 PRELIMINARY; PRT; 371 AA.
 AC Q9HC73:
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE CYTOKINE RECEPTOR CRL2 PRECURSOR (IL-XR) (THYMIC STROMAL LYMPHOPOIETIN
 DE PROTEIN RECEPTOR TSLP).
 GN CRL2 OR IL-XR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBL_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21134329; PubMed=11237741;
 RA Zhang W., Wang J., Wang Q., Chen G., Zhang J., Chen T., Wan T.,
 RA Zhang Y., Cao X.;
 RT "Identification of a novel type I cytokine receptor CRL2
 RT preferentially expressed by human dendritic cells and activated
 RT monocytes.";
 RT Blochem. Biophys. Res. Commun. 281:878-883(2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Tonozeuka Y., Fujio K., Sugiyama T., Nosaka T., Hirai M., Kitamura T.;
 RT "Molecular cloning of a human novel type I cytokine receptor related
 RT to Delta.";
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311890; PubMed=11418668;
 RA Reche P.A., Soumelis V., Gorman D., Menon S., Zurawski S.,
 RA Johnston J., Liu Y.-J., Spits H., de Waal-Malefyt R., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Human thymic stromal lymphopoietin preferentially stimulates myeloid
 RT cells.";
 RL J. Immunol. 167:336-343(2001).

DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR Pfam: PF00041; fn3; 1.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
 KM Signal: Receptor.
 FT SIGNAL 1 17
 FT CHAIN 18 415
 FT SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 10.7%; Score 137.5; DB 11; Length 415;
 Best Local Similarity 23.3%; Pred. No. 4.5e-05;
 Matches 54; Conservative 41; Mismatches 102; Indels 35; Gaps 11;

QY 8 PNGEDTTADFLITMTPTDLSVSTPLPEVQCFFVNEVMCTNNSSSE-PQPTNLTLLH 66
 DB 118 PGSPGTSIVLACTTNTAASNYTLKSYVS-----LHCTWLACGADPEDTQYFLY 169
 DB 67 YWYKNSNDKVKCKSHLSEELTS--GCQLQKKEIH--LYQTFVYQLODPRPRKQAT 121
 DB 170 YRY---GPTWEECOEY--SKDPLSRNTACWPPRTFTHSKARDRLAVHVG--SSNHA 220
 QY 122 -----QMLKLNLYIPWAPENLTLLHKLSESOLELNN--NRLNCHLEHLYQRTDMDH 173
 DB 221 IKPFQQLFDQALDQNPMPDVTAT-ETEGSRSLSLQWQKPYSAPIHCFEYVATCTKDY 279
 QY 174 SMTQSDYDVKHKSPLPSVDQKRTFRVRSRFPDLGSAQHSMSHPHMG 225
 DB 280 YQVEKTTT---NAFVSTTDGVSRTSIQVRAVSPHCRAMGLMSKMSQPYVVG 328

RESULT 11
 ID 057519 PRELIMINARY; PRT; 881 AA.
 AC 057519;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP130P1.
 GN XGP130.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 PP SEQUENCE FROM N.A.
 CH Chen J., Grace A., Chien K.R.;
 ST Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF041845; AAC03531.1; -.
 DR HSSP; P40189; 1B0U.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 10.7%; Score 137.5; DB 13; Length 881;
 Best Local Similarity 23.3%; Pred. No. 0.00011;
 Matches 51; Conservative 31; Mismatches 94; Indels 43; Gaps 10;
 QY 18 FFLTMTPTDLSVSTPLPEVQCFFVNEVMCTNNSSSE-PQPTNLT--HYWYKSDND 75
 DB 115 FFLTGEPDPEPT-----NLTCIVYNODMLCTMDPGRPNTNPTVYTLSHMAHFGAN- 166
 QY 76 KYVCKSHYLESEELTSCQLQKKEIHLYQTFVYQLODPRPRKQATQMLKLO--NLVYIW 133
 DB 167 -----YCRGANSNSTHSPGFYIDTTFQVEATNELGIQKSELTLLDPVNTVKN 217

QY 134 APENTLLHKLSE-----SOLELNNMNRFLN-HCLEHLYQYR---TMDHSWTEQSY 180
 DB 218 PPG-----LSELLSSLELPAALKIEMKNPTTNMFLNKYRNPVPTQDMENVPEBDTA 271
 QY 161 DYRKFSPLPSVDGQKRTFRVRSRFPDLGSAQHSMS 219
 DB 272 SHRDSFTLQDILLPNTVEVSIRCIHKDHG---FWSWDS 307

RESULT 12
 ID 097597 PRELIMINARY; PRT; 349 AA.
 AC 097597;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 PP SEQUENCE FROM N.A.
 RA MEDLINE=20080132; PubMed=10614495;
 RA Triglona W.L., Brown W.C., Estes D.M.;
 RT functional implications for signaling via the IL4R/IL13R complex on
 RT bovine cells.";
 RL Vet. Immunol. Immunopathol. 72:73-79(1999).
 DR EMBL; AF074402; AAC98147.1; -.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
 KM Receptor.
 FT NON_TER 1 1
 FT NON_TER 349 349
 SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 10.6%; Score 137; DB 6; Length 349;
 Best Local Similarity 24.0%; Pred. No. 4.1e-05;
 Matches 52; Conservative 37; Mismatches 98; Indels 30; Gaps 11;
 QY 38 VOCEFFVNEVMCTW---NSSSEPOPTNLTLYWYKNSNDKVKCKSH-YLFSEELTSG 92
 DB 98 LQCTIHNLRVYKCKTWLPERNASPPD---NYLLVYHNSL--GRIQCENYREGQHIACS 152
 QY 93 CQLOKKEIHLYQTYVQ--LDDPRPRKQATQMLKLNLYIPWAPENLTLLHKLSESOLE 150
 DB 153 FNLRKVKNSSEQHSQVQVMDNAGKISPSFNIVPLTSHVKP--DPSHIKMLSFQNGDLVY 211
 QY 151 MNWN--RFLNHCL-----EHLVQYRTDMDHSWTE-----QSDVYRNK-----FSLPSVDQ 194
 DB 212 QNTNPNQNSQCLCEVEVINSNAETHTDIFYEAKQKQNTPEFEGNEGTICFMVPGVLD 271
 QY 195 KRYTFRVRSRFPNPLC-GSAQHSMSHPHMGNTSK 230
 DB 272 TLNTVTRIRKTKKLCYEDDKLMSNMQAMSIGOKANQ 308
 RESULT 13
 ID 064146 PRELIMINARY; PRT; 896 AA.
 AC 064146;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
 GN IL-3R<BETA>
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;

RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95370942; PubMed=7643220;
 RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
 RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
 RL microglia and its mRNA expression in vivo."; J. Neurosci. 15:5800-5809(1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE=BRAIN;
 RA Gebicke-Haerter P.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: S79263; AAB35068.1; -;
 DR EMBL: AJ000555; CA04186.1; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR00282; CytoK_receptor_2.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 FT SIGNAL.
 FT NON_TER
 SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 10.6%; Score 136.5; DB 11; Length 896;
 Best Local Similarity 23.9%; Pred. No. 0.00014;
 Matches 48; Conservative 41; Mismatches 83; Indels 29; Gaps 11;
 QY 38 VOCFVFNVEYNKCTWNSSEPOPTNLTHVYKNSDNDKVKCSHYLFSEITSG----- 92
 DB 251 LQCFEGIOISLCSNCEWMTK-VTDSVSGFLGFLSSSPKAGEKKCSYV--KELQASRYTRY 307
 QY 93 -COLQKEITHLYQTFFVVOLODPRPRROATQMLKQNLVIFWAPENLTLKLSQLELN 151
 DB 308 HCSLNVSPDAHSAQYTSVK-----RLQGRFIESFN-HIQNPPTLTLNTRNS-VSLH 360
 QY 152 WNNR-----FLNHCLEHLVQYRTD--MDHSWTEQSDYRKKEFSLPVYGOKRYTFYRVS 203
 DB 361 METQKMSYFIFQIAFO--VQYKKKIDRWEDSKTE-NLNAHSMQLPQLEPGTSICARVY 417
 QY 204 RNPPLGSAQHWSEWSHPITW 224
 DB 418 KTIPEYKGL--WSEWSNCEWTW 436

RESULT 14
 5R3
 09H5R3 PRELIMINARY; PRT; 232 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CDNA: FLJ23147 FIS, CLONE LMG09295.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Kawakami T., Nouguchi S., Itoh T., Shigetani K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Harao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Iisega T., Sugano S.;
 RT "NEO human cDNA sequencing project";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK026800; BAB15557.1; -;
 SQ SEQUENCE 232 AA; 26703 MW; 56946BE74C226F5 CRC64;

Query Match 10.6%; Score 136; DB 4; Length 232;
 Best Local Similarity 23.1%; Pred. No. 3.2e-05;
 Matches 55; Conservative 33; Mismatches 54; Indels 96; Gaps 13;
 QY 37 EVOCFVFNVEYNKCTWNSSEPOPTNLTHVYKNSDNDKVKCSHYLFSEITSGCOL- 95
 DB 30 QIOIIFNLETQVYVWNAKSKSR-TNLPFHYRF-NGD-EAYDQCTNYLLOGGHTSGCLLD 86
 QY 96 -OKKEITHLY-----QTFVVOLODPRPRROATQMLKQNLVIFWAPENLTLH 141
 DB 87 AEGRDILIFSRINGTHPVFTASRMWVYLLKSPSK-----HYRFSWHDQAVTV- 135
 QY 142 KLSQLELNMMNNRFLNHCLEHLVQYRTDHSWTEQ----- 178
 DB 136 ---TCSDSLSTGPD-----LLYEVOYRSPFDPEWQTSKSVTQACVQWCDLCLQSPPR 185
 QY 179 -----SVDYRH-----KESLPVSDGOKRYTFYRVSFRPNPLGSAQHWSEWS 219
 DB 186 KRFPSCLSLPSSWDYRHPRLANFCIISRDC-----VSP-C-----WPGWS 226

RESULT 15
 09IBF6
 ID 09IBF6 PRELIMINARY; PRT; 611 AA.
 AC 09IBF6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROLACTIN RECEPTOR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE=20289252; PubMed=10830440;
 RA Yamamoto T., Nakayama Y., Abe S.-I., Kawahara A.;
 RT "Cloning of cDNA for Xenopus prolactin receptor and its morphologic
 RT expression profile."; J. Dev. Growth Differ. 42:167-174(2000).
 RL EMBL: AB030443; BA090400.1; -;
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
 KW RECEPTOR.
 SQ SEQUENCE 611 AA; 68315 MW; 7E0DE76F21D8CE97 CRC64;

Query Match 10.1%; Score 130; DB 13; Length 611;
 Best Local Similarity 24.7%; Pred. No. 0.00037;
 Matches 59; Conservative 36; Mismatches 100; Indels 44; Gaps 13;
 QY 2 NNTILPNGNEDTADFFLTTPDLSVSTPLDPEV--QCFVFNVEYNKCTWNSSE-P 58
 DB 4 NLAPTP-----SVAVTFLFLTYVSLNAOSLPGRVIDIKCRSEYKRYFSGWKKGSDGG 58
 QY 59 OPTNLTHVYKNSDNDKVKCSHYLFSEITSG---COLQKE-----THLYQTFVVO 109
 DB 59 LPTNYSL--LYRKENPDKTYECPDY-----VTSGLNSCFPKAHKSPVTFHYIY--VN 107
 QY 110 LODPRPRROATQMLKQNLVIFWAPENLTLH-KLSQLELNW-----NNRFLNHC 160
 DB 108 ATNALNSVNSDESVDPTTYIVQYPTPTVNSLAVESGHHDLKMLPRAWVDVQSGMLT- 165
 QY 161 LEHLVQYRTDHSWTEQSDYRHKFSLSPVDGOKRYTFYRVSRRNPPLGSAQHWSEWS 219
 DB 166 LKYEVRKEKEQEWENHVLVGNQLKRLGLTPGNGYVVOVRC--PDSG--HWSEWS 219

Fri, Jun 28 07:58:59 2002

us-09-825-561a-4.rspt

Page 7

Search completed: June 28, 2002, 07:44:30
Job time: 225 sec

Fri Jun 28 07:58:59 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:46:27 ; Search time 110.69 Seconds

(without alignments)
218.756 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195

Sequence: 1 CPDLVCYTDVLTQVICILEM.....SDPVIRQTQSEELKEGWNPH 218

Scoring table:

BLOSUM62
Gapop 10.0 , Gapect 0.5

rched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_032802:*

- 1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
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- 19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
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- 22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	289	21	AAV45029
2	1195	100.0	361	21	AAV69883
3	1195	100.0	538	20	AAV27450
4	1195	100.0	538	21	AAH18634
5	1195	100.0	538	21	AAV79312
6	1195	100.0	538	21	AAV45031
7	1195	100.0	538	22	AAV69886
8	1195	100.0	538	22	AAH48001
9	1195	100.0	606	21	AAH18629
10	1195	100.0	606	21	AAV79316
11	1188	99.4	538	21	AAV94304

12	1188	99.4	538	22	AAU08728	Human HNOVILR poly
13	1187	99.3	471	21	AAV45030	HUMAN OCR10-Fc fus
14	1170	97.9	538	22	AAE02459	Human DNAX cytokin
15	1159	97.0	538	21	AAV69888	Mouse haemopoietin
16	1145	95.8	460	21	AAV69890	Human haemopoietin
17	1138	95.2	375	21	AAV69889	Human NR8alpha/IgG
18	1077	90.1	568	21	AAV94305	Human NR8alpha/TP0
19	1077	90.1	568	22	AAV94305	Human HNOVILR poly
20	1077	90.1	568	22	AAU08729	Human HNOVILR poly
21	844	70.6	529	21	AAE02457	Human DNAX cytokin
22	838	70.1	529	21	AAV79320	Mouse cytokine rec
23	548	45.9	158	21	AAH48002	Murine IL-9/IL-2 r
24	543.5	45.5	144	21	AAV69891	Human NR8beta/FLAG
25	521.5	43.6	144	21	AAV69884	Human haemopoietin
26	400	33.5	397	21	AAV79319	Mouse haemopoietin
27	362	30.3	227	21	AAV69885	Mouse cytokine rec
28	176	14.7	57	22	AAV69885	Human haemopoietin
29	176	14.7	57	22	ABH39255	Peptide #6761 enco
30	176	14.7	57	22	ABH24090	Protein #6089 enco
31	176	14.7	57	22	AAV59919	Human brain expres
32	176	14.7	57	22	AAV72513	Human bone marrow
33	176	14.7	57	22	AAV19611	Peptide #6045 enco
34	148	12.4	878	17	AAV32757	Peptide #6794 enco
35	145	12.1	576	16	AAV92529	Fas sequence from
36	145	12.1	576	16	AAV78613	Expression vector
37	145	12.1	592	17	AAV92527	Fas antigen #2. S
38	145	12.1	596	16	AAV78616	Expression vector
39	145	12.1	600	17	AAV78610	Expression vector
40	145	12.1	600	17	AAV92526	Fas antigen #1. S
41	144.5	12.1	539	11	AAV78608	Murine IL-3 recept
42	144	12.1	539	11	AAV78608	Murine interleukin
43	144	12.1	783	18	AAV24054	Murine WsX recepto
44	144	12.1	805	18	AAV22102	Murine WsX recepto
45	144	12.1	894	18	AAV24064	Murine WsX recepto

ALIGNMENTS

RESULT 1	AAV45029	standard; Protein; 289 AA.
ID	AAV45029	
XX	AAV45029;	
AC		
XX		
DT	31-MAY-2000	(first entry)
XX		
DE	HUMAN Orphan Cytokine Receptor-10 (OCR10) polypeptide.	
XX		
KW	Human; Orphan Cytokine Receptor-10; OCR10; chromosome 16p12;	
KW	cytokine; screen; cognate ligand; treatment; endocrine disorder;	
KW	immune disorder.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	4..21
FT		/label= Signal_peptide
FT	Protein	22..289
FT		/label= Mature_HUMAN_OCR10
FT	Region	118..169
FT		/label= Proline_hinge_motif_region
FT	Domain	122..123
FT		/label= Proline_hinge_motif
FT		238..255
FT		/label= Transmembrane_domain
FT		/note= "Putative and hydrophobic"
FT	Region	263..278
FT		/label= Jak-binding_region
XX		/note= "potential"
PN	W0200008152-A1.	
XX		

PD 17-FEB-2000.
 XX
 PF 16-JUL-1999; 99WO-US16060.
 XX
 PR 04-AUG-1998; 98US-0128820.
 XX
 PA (REGC-) REGENERON PHARM INC.
 XX
 PI Maslakowski PJ, Morris J, Valenzuela DM;
 XX
 DR WPI; 2000-205707/18.
 DR N-PSDB; AA250746.
 XX
 PT New HUMAN orphan cytokine receptors 10 and 10-A useful for screening
 PT for drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands
 PS
 PS Example 1; Page 21; 54pp; English.
 CC The present sequence is the HUMAN Orphan Cytokine Receptor-10
 CC (OCRI10) polypeptide. HUMAN OCRI10 gene is located on chromosome 16p12.
 CC It is expressed at high levels in spleen, thymus, peripheral blood
 CC leucocytes and lymph nodes and moderately in heart and placenta. It
 CC has a role in immune system and cytokine function. It is useful in
 CC screening for cognate ligands or drugs that mediate survival and
 CC differentiation of cells expressing this receptor. Modified HUMAN
 CC OCRI10 or its agonist can be used in the treatment of endocrine or
 CC immune disorders.
 CC
 XX Sequence 289 AA:
 SQ

Query Match 100.0%; Score 1195; DB 21; Length 289;
 Best Local Similarity 100.0%; Pred. No. 6.4e-116;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLYQIVYICILEMNNLHPSTLTLTWQDYELKDEATSCSLHSAHNATHATY 60
 DB 20 CPDLVCTDYLYQIVYICILEMNNLHPSTLTLTWQDYELKDEATSCSLHSAHNATHATY 79
 QY 61 TCHMDVFFHMADDFISVNTDQSGNYSOECGFFLAESIKPAPFNTVTFTSGQYNISMR 120
 DB 80 TCHMDVFFHMADDFISVNTDQSGNYSOECGFFLAESIKPAPFNTVTFTSGQYNISMR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 199
 DB 181 VRAGPMGSSYOGTMSWSDPVIRFOTQSEELKEGMNPH 218
 200 VRAGPMGSSYOGTMSWSDPVIRFOTQSEELKEGMNPH 237

RESULT 2
 AAY69883
 ID AAY69883 standard; Protein; 361 AA.
 XX
 AC AAY69883;
 XX
 DT 24-MAY-2000 (first entry)
 XX
 DE Human haemopoietin receptor family member NR8alpha.
 XX
 KW Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder.
 OS Homo sapiens.
 OS
 PN WO967290-A1.
 XX
 PD 29-DEC-1999.
 XX

PF 23-JUN-1999; 99WO-JP03351.
 XX
 PR 24-JUN-1998; 98JP-0214720.
 PR 19-OCT-1998; 98JP-0237409.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PI Nomura H, Maeda M;
 XX
 DR WPI; 2000-116933/10.
 DR N-PSDB; AA259237.
 XX
 PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -
 PS
 PS Claim 1; Fig 5-6; 176pp; Japanese.
 CC This sequence represents a novel haemopoietin receptor protein family
 CC NR8, designated NR8alpha. Antibodies to the NR8 family proteins are used
 CC for the diagnosis of blood formation disorders. Compounds identified as
 CC binding to the proteins are used for the treatment of such disorders.
 CC
 XX Sequence 361 AA:
 SQ

Query Match 100.0%; Score 1195; DB 21; Length 361;
 Best Local Similarity 100.0%; Pred. No. 8.8e-116;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLYQIVYICILEMNNLHPSTLTLTWQDYELKDEATSCSLHSAHNATHATY 60
 DB 20 CPDLVCTDYLYQIVYICILEMNNLHPSTLTLTWQDYELKDEATSCSLHSAHNATHATY 79
 QY 61 TCHMDVFFHMADDFISVNTDQSGNYSOECGFFLAESIKPAPFNTVTFTSGQYNISMR 120
 DB 80 TCHMDVFFHMADDFISVNTDQSGNYSOECGFFLAESIKPAPFNTVTFTSGQYNISMR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMGSSYOGTMSWSDPVIRFOTQSEELKEGMNPH 218
 DB 200 VRAGPMGSSYOGTMSWSDPVIRFOTQSEELKEGMNPH 237

RESULT 3
 AAY27450
 ID AAY27450 standard; Protein; 538 AA.
 XX
 AC AAY27450;
 XX
 DT 26-NOV-1999 (first entry)
 XX
 DE Human MU-1 hematoopoietin receptor protein.
 XX
 KW MU-1 hematoopoietin receptor protein; gene therapy;
 KW cell proliferation; cytokine production; immune response; cancer;
 KW autoimmune disease; transplant rejection; hematoopolesis; anemia;
 KW gene mapping; nutritional supplement; human.
 OS Homo sapiens.
 OS
 PN WO9947675-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99WO-US05854.
 XX
 PR 17-MAR-1998; 98US-0040005.
 XX
 PA (GEMY) GENETICS INST INC.
 XX

PI Donaldson D, Ungar M;

XX WPI: 1999-562115/47.

DR N-PSDB; AA207535.

XX New nucleic acid encoding the MU-1 hematopoietin receptor protein, used
PT for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis
PI

PS Claim 9; Page 33-35; 37pp; English.

XX This represents a MU-1 hematopoietin receptor protein. The protein can
CC be produced by standard recombinant methodology. The MU-1 protein has the
CC biological activity of the MU-1 hematopoietin receptor superfamily chain.
CC It is used to screen for specific binding agents; to raise specific
CC antibodies; as assay reagents, tissue markers etc. and therapeutically
CC (optionally expressed from the MU-1 gene by gene therapy). Many possible
CC activities/uses of the MU-1 protein are described without supporting
CC evidence, e.g. they regulate cell proliferation and differentiation,
CC induce production of cytokines, stimulate or suppress an immune response
CC (e.g. for treating immune deficiency of any etiology, cancer or
CC autoimmune disease, and for preventing transplant rejection) and regulate
CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
CC research reagent, for recombinant production of the protein, as tissue or
CC molecular weight marker, for gene mapping; for production of anti-DNA or
CC anti-protein antibodies etc. The MU-1 protein and the nucleic acids are
CC also useful as nutritional supplements or sources and the antibodies can
CC be used therapeutically, as assay reagents and for affinity purification.
XX

SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 20; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.6e-115; Indels 0; Gaps 0;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLOTVICILEMMNLHPSTLTLTWQDOYEELKDEATCSLHRSANATHATY 60

DB 20 cpdlvcytdyqltvicillemmnlhpsltltltwqdyeelkdeatcslnhsanathaty 79

QY 61 TCHMDVFNHADDISVNTTDSGNYSCGCSFLAESIKPAPPNVYVTFSSQYINISMR 120

DB 80 tchmdvfnhaddisvntldsgnyscgcsflaesikpappfnvtfvtfssqynlswr 139

QY 121 SDYEDPAFMYMKGLQYELQYRNKGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180

DB 140 sdyedpafmylmgklyelqyrnkgdpwavsprkllsvdsrsvsllplefrkdsseyelq 199

QY 181 VRAGPMGSSYOGTWSWSDPVIFOTOSSELKEGNNPH 218

DB 200 vragpmpgssyqgtwsewscpvilftqseelkegnph 237

RESULT 4 AAB18634 standard; Protein; 538 AA.

AC AAB18634;

DT 22-JAN-2001 (first entry)

DE A human zalphal1 ligand polypeptide.

KM zalphal1 ligand; cytokine; haematopoietic cell proliferation; lymphoma;

KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

OS Homo sapiens.

PN WO200053761-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000MO-US06067.

XX 09-MAR-1999; 99US-0264908.

PR 11-MAR-1999; 99US-0265992.

PR 01-JUL-1999; 99US-0142013.

PA (ZYMO) ZYMOGENETICS INC.

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;

PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

DR WPI: 2000-565600/52.

DR N-PSDB; AAA75557.

PT New human cytokine, designated zalphal1 ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
PT and in vivo, and for treating tumorigenesis -

PS Disclosure; Page 255-256; 256pp; English.

XX The present sequence represents a human zalphal1 ligand polypeptide,
CC which is a cytokine. The zalphal1 ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphal1 ligand polynucleotides can be used as primers or probes
CC for cloning the zalphal1 gene. The zalphal1 ligand is useful for
CC treating tumorigenesis. A zalphal1 ligand-saporin fusion toxin may be
CC used for treating leukemias and lymphomas. Antagonists against zalphal1
CC ligand are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphal1 ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphal1 polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphal1 ligand
CC genetic defect.
XX

SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 21; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.6e-115; Indels 0; Gaps 0;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLOTVICILEMMNLHPSTLTLTWQDOYEELKDEATCSLHRSANATHATY 60

DB 20 cpdlvcytdyqltvicillemmnlhpsltltltwqdyeelkdeatcslnhsanathaty 79

QY 61 TCHMDVFNHADDISVNTTDSGNYSCGCSFLAESIKPAPPNVYVTFSSQYINISMR 120

DB 80 tchmdvfnhaddisvntldsgnyscgcsflaesikpappfnvtfvtfssqynlswr 139

QY 121 SDYEDPAFMYMKGLQYELQYRNKGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180

DB 140 sdyedpafmylmgklyelqyrnkgdpwavsprkllsvdsrsvsllplefrkdsseyelq 199

QY 181 VRAGPMGSSYOGTWSWSDPVIFOTOSSELKEGNNPH 218

DB 200 vragpmpgssyqgtwsewscpvilftqseelkegnph 237

RESULT 5 AA79312 standard; Protein; 538 AA.

AC AA79312;

DT 18-JUL-2000 (first entry)

DE Human cytokine receptor zalphal1.

KM Cytokine receptor; zalphal1; human; chromosome 16p11.1;

KW apoptosis; signal transduction; growth factor; cancer; tumour;
infection; immunosuppressive; immunostimulant; autoimmune disease;

KM Leukaemia; lymphoma; transplant rejection; therapy; diagnosis.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..538
 FT /note= "mature protein: a polypeptide comprising the mature protein is specifically claimed in Claim 27(d)"
 FT Region 214..218
 FT /note= "WSXWS motif"
 FT Domain 20..237
 FT /note= "cytokine-binding domain: a polypeptide comprising this domain is specifically claimed in Claim 27(a)"
 FT Domain 192..202
 FT /note= "penultimate strand region"
 FT Domain 238..255
 FT /note= "transmembrane domain"
 FT Domain 256..538
 FT /note= "intracellular signalling domain; a polypeptide comprising this domain is specifically claimed in Claim 27(c)"
 FT Region 267..273
 FT /note= "Box I signalling site"
 FT Region 301..304
 FT /note= "Box II signalling site"
 XX WO200017235-A2.
 PD 30-MAR-2000.
 XX 23-SEP-1999; 99WO-US22149.
 XX 23-SEP-1999; 98US-0159254.
 PR 09-MAR-1999; 99US-0265117.
 PR 06-JUL-1999; 99US-0347930.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Presnell SR, Conklin DC, Novak JE, Hammond AK;
 PI WPI, 2000-292825/25.
 DR N-PSDB: AA294533, AA294534.
 XX Novel nucleic acid encoding zaiphal1 polypeptide, useful for treating e.g. viral infection or tumors, and for identifying ligands that stimulate cell proliferation -
 PT Claim 27(e); Page 148-149; 190pp; English.
 XX The present sequence is that of zaiphal1, a novel human class I
 CC cytokine receptor that may be involved in an apoptotic cellular
 CC pathway, or is a cell-cell signalling molecule, growth factor
 CC receptor, or extracellular matrix associated protein with growth
 CC factor hormone activity. The sequence was deduced from a cDNA clone
 CC (see AA294533) isolated from a spinal cord library. Polypeptides
 CC comprising amino acids 20-237, 20-255, 256-538, 20-538 and 1-538 of
 CC the present sequence are claimed. zaiphal1 is expressed in lymph
 CC node, peripheral blood leucocytes, spleen and thymus. The mRNA is
 CC also abundant in the Raji cell line (ATCC CCL 86) derived from
 CC Burkitt's lymphoma. Zaiphal1 polypeptides, and fusion proteins
 CC including them, can be obtained by expression in recombinant host
 CC cells. They are used: to detect ligands (also ligand agonists and
 CC antagonists) that stimulate proliferation and/or development of
 CC haematopoietic, lymphoid and myeloid cells, in vitro or in vivo,
 CC e.g. as a replacement for serum in culture media; in soluble form
 CC to block ligand activity (direct antagonists) and to detect
 CC ligand-expressing cancers; to raise specific antibodies; and for
 CC purification of cognate ligands. Agonistic ligands may stimulate
 CC cell-mediated immunity, e.g. for treating (viral) infections

CC associated with immunosuppression, improving the activity of
 CC vaccines, suppressing tumours, treating leukaemia and improving
 CC T-cell regeneration after bone marrow transplant. Antagonists are
 CC useful as immunosuppressants, e.g. in the treatment of autoimmune
 CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes),
 CC to prevent transplant rejection and to treat T-cell leukemia or
 CC lymphoma.
 XX Sequence 538 AA:
 SQ
 Query Match 100.0%; Score 1195; DB 21; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCTYDYIQTIVYCIEMNNLHPSTLTWQOYELKDEATSCSLHSAKHATATY 60
 DB |||||||
 DB 20 cpdlvcytdyiqtyvcillemnlhpsltltwqdyeeldeatscslhsahnataty 79
 QY 61 TCHMDVFHMDIDFVSVNTDQSGNYSQCGSFLLAESIRPAPFNTVTFSGQYNSMR 120
 DB |||||||
 DB 80 tchmdvfimddlfsvntdqsngysqcgslfaeslkpappfnvtvtfsgynlswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDSRVSLLPLEFRKDSYEIQ 180
 DB |||||||
 DB 140 sdyedpatfymkglkyelqyrnrgdpwavsprkllsvdsrsvllplefrkdsyeld 199
 QY 181 VRAGPMGSSYQGTWSEMSDPVITOTQSEELKEGMNH 218
 DB |||||||
 DB 200 vragpmpgssyqgtwsemsdpvltqseelkegmnh 237
 RESULT 6
 AAY45031
 ID AAY45031 standard; Protein: 538 AA.
 XX AAY45031;
 AC
 XX 31-MAY-2000 (first entry)
 DT
 XX HUMAN Orphan Cytokine Receptor 10 (OCR10)-A polypeptide.
 DE
 XX Human; Orphan Cytokine Receptor 10-A; OCR10-A: cytokine; screen;
 KW cognate ligand; treatment; endocrine disorder; immune disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200008152-A1.
 PD 17-FEB-2000.
 XX 16-JUL-1999; 99WO-US16060.
 XX 04-AUG-1998; 98US-0128820.
 PR (REGF-) REGENERON PHARM INC.
 XX Maslakowski PJ, Morris J, Valenzuela DM;
 PI WPI: 2000-205707/18.
 DR N-PSDB: AA250748.
 XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening
 PT for drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands
 XX Example 10; Page 39-41; 54pp; English.
 PS
 XX The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A
 CC (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus,
 CC peripheral blood leucocytes and lymph nodes and moderately in heart and
 CC placenta. It has a role in immune system and cytokine function. It is

CC useful in screening for cognate ligands or drugs that mediate survival
CC and differentiation of cells expressing this receptor. Modified HUMAN
CC OCRI0-A or its agonist can be used in the treatment of endocrine or
CC immune disorders.
XX
SQ Sequence 538 AA:

Query Match 100.0%; Score 1195; DB 21; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQTVICILEMWNLPSTLTITWODYEELKDEATSCSLRSHAHNATHATY 60
DB 20 CPDLVCTDYLTQTVICILEMWNLPSTLTITWODYEELKDEATSCSLRSHAHNATHATY 79
QY 61 TCHMDVFHMADDFSVNITDQSGNSQECGSFLAESIKPAPPNVTVTFSGQYNISM 120
DB 80 TCHMDVFHMADDFSVNITDQSGNSQECGSFLAESIKPAPPNVTVTFSGQYNISM 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGPMAVSPRRKLISVDSVSLPLEFKDSSYLEQ 180
DB 140 SDYEDPAFYMLKGLQYELQYRNKGPMAVSPRRKLISVDSVSLPLEFKDSSYLEQ 199
QY 181 VRAGPMGSSYOGTSEMSDPVIFQTQSEELKEGMNPH 218
DB 200 VRAGPMGSSYOGTSEMSDPVIFQTQSEELKEGMNPH 237

RESULT 7

AA69886
ID AAB69886 standard; Protein; 538 AA.

AC AAB69886;

DT 24-MAY-2000 (first entry)

DE Human haemopoietin receptor family member NR8gamma.

KM Haemopoietin receptor family; NR8; antibody; diagnosis;

KW blood formation disorder.

OS Homo sapiens.

PN WO967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Nomura H, Maeda M;

DR WPI: 2000-116933/10.

DR N-PSDB; AAZ59240.

PT Hemopoietin receptor protein family NR8 used for diagnosis of blood

PT formation disorders -

PS Claim 4; Fig 9-10; 176pp; Japanese.

CC This sequence represents a novel haemopoietin receptor protein family

CC NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used

CC for the diagnosis of blood formation disorders. Compounds identified as

XX binding to the proteins are used for the treatment of such disorders.

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 21; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQTVICILEMWNLPSTLTITWODYEELKDEATSCSLRSHAHNATHATY 60
DB 20 CPDLVCTDYLTQTVICILEMWNLPSTLTITWODYEELKDEATSCSLRSHAHNATHATY 79
QY 61 TCHMDVFHMADDFSVNITDQSGNSQECGSFLAESIKPAPPNVTVTFSGQYNISM 120
DB 80 TCHMDVFHMADDFSVNITDQSGNSQECGSFLAESIKPAPPNVTVTFSGQYNISM 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGPMAVSPRRKLISVDSVSLPLEFKDSSYLEQ 180
DB 140 SDYEDPAFYMLKGLQYELQYRNKGPMAVSPRRKLISVDSVSLPLEFKDSSYLEQ 199
QY 181 VRAGPMGSSYOGTSEMSDPVIFQTQSEELKEGMNPH 218
DB 200 VRAGPMGSSYOGTSEMSDPVIFQTQSEELKEGMNPH 237

RESULT 8

AAB48001
ID AAB48001 standard; Protein; 538 AA.

AC AAB48001;

DT 19-MAR-2001 (first entry)

DE Human IL-9/IL-2 receptor-like 16445 protein.

XX Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;

KW T-lymphocyte-related disorder; antiarthritic; antipsoriatic; human;

KW immunosuppressive; antiasthmatic; antiallergic; antithyroid; cytostatic;

KW antiarthritic; nephrotropic; gene therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19 /note="signal peptide"

FT Protein 20..538 /note="mature protein"

PN WO200069880-A1.

XX 23-NOV-2000.

XX 18-MAY-2000; 2000WO-US13687.

XX 18-MAY-1999; 99US-0313913.

PA (MILL-) MILLENNIUM PHARM INC.

PI Hodge MR;

DR WPI: 2001-016209/02.

DR N-PSDB; AAC84147.

PT Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for

PT diagnosis and treatment immune, inflammatory and respiratory disorders

PT and in screening assays for identifying modulators -

PS Claim 8; Page 104-106; 119pp; English.

CC The invention relates to isolated human and murine interleukin-9 (IL-9)
CC /IL-2 receptor-like polypeptides. The plasmid containing the encoding
CC cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like
CC polypeptides (16445 proteins) can be recombinantly produced using
CC standard recombinant methodology. The 16445 proteins are used for
CC identifying their modulators and for diagnosis and treatment of immune,
CC inflammatory and respiratory disorders and disorders associated with
CC lungs, colon, kidney and lymphoid tissues including tonsil and thymus,

CC in particular T-lymphocyte-related disorders including atopic conditions
 CC such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic
 CC inflammatory diseases and graft versus host disease, disorders involving
 CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
 CC disorders including polycystic kidney disease, cystic renal dysplasia,
 CC disorders of the thymus including lymphomas, Hodgkin disease and
 CC carcinoids. The 1643 polypeptides are also useful as modulating agents
 CC in cellular processes including growth promoting activity, particularly
 CC the antigen-independent proliferation of T-helper cell clones. The
 CC encoding nucleic acid is useful as primers or hybridization probes for
 CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
 CC tissue typing and in forensic biology. The present sequence represents
 CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445).

XX
 SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 22; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYLTQIVICILEMNNLHPSTLTITWODYEELKDEATSCSLHRSAHNTHATY 60
 |||||||
 Db 20 cpdlvctdyltqivicilemnnlhpsltltitwgdyeelkdeatscslhrsahnathty 79

QY 61 TCHMDVHFHMADDFSVNITDQSGNSOEGSFLAESIKRPAPFNWVTFSGOYNISMR 120
 |||||||
 Db 80 tchmdvfhmaddfsvnitdsgnysgecgstllaesikpappfnvtfisgyniswr 139

QY 121 SDYEDPAFYMLKGLKLOYEYRNKGDPMWVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 |||||||
 Db 140 sdyedpafymkglklyelgyrnrgdpwvsprkllsvdsrsvsllplefrkdsseyelq 199

QY 181 VRAGPMGSSYOGTSEMSDPVIFQOSEELKEGMNPH 218
 |||||||
 Db 200 vragpmpgssyogtsemsdpvifqtqseelkegmnp 237

RESULT 9
 AAB18629
 ID AAB18629 standard; Protein; 606 AA.

XX AAB18629;
 DT 22-JAN-2001 (first entry)

XX Amino acid sequence of MBP-human zalphall ligand fusion.
 DE zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
 XX tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
 KW

OS Synthetic.
 XX Homo sapiens.

PN WO200053761-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-US06067.

PR 09-MAR-1999; 99US-0264908.

PR 11-MAR-1999; 99US-0265992.

PR 01-JUL-1999; 99US-0142013.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
 PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

DR WPI: 2000-565600/52.

DR N-PDB: AAA75609.

PT New human cytokine, designated zalphall ligand, useful for stimulating

PT the proliferation and/or development of haematopoietic cells in vitro
 PT and in vivo, and for treating tumorigenesis -
 XX

PS Example 45; Page 245-247; 256pp; English.

XX The present sequence represents a MBP-human zalphall ligand fusion.
 CC zalphall ligand is a cytokine. The zalphall ligand is useful for
 CC stimulating the proliferation and development of haematopoietic cells
 CC in vitro and in vivo. zalphall ligand polynucleotides can be used as
 CC primers or probes for cloning the zalphall gene. The zalphall ligand
 CC is useful for treating tumorigenesis. A zalphall ligand-saporin fusion
 CC toxin may be used for treating leukaemias and lymphomas. Antagonists
 CC against zalphall ligand are useful as research reagents for also useful
 CC characterizing ligand-receptor interaction. Antagonists are also useful
 CC for inhibiting expansion, proliferation, activation and differentiation
 CC of cells involved in regulating hematopoiesis. The zalphall ligand may
 CC also be used to stimulate an immune response against B cell tumour, a
 CC virus, a parasite or a bacterium. The zalphall polypeptides,
 CC polynucleotides, antagonists, agonists and antibodies are also useful
 CC for the detection, diagnosis, prognosis, prevention, and treatment of diseases
 CC associated with a zalphall ligand genetic defect.

XX Sequence 606 AA;

Query Match 100.0%; Score 1195; DB 21; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQIVICILEMNNLHPSTLTITWODYEELKDEATSCSLHRSAHNTHATY 60
 |||||||
 Db 389 cpdlvctdyltqivicilemnnlhpsltltitwgdyeelkdeatscslhrsahnathty 448

QY 61 TCHMDVHFHMADDFSVNITDQSGNSOEGSFLAESIKRPAPFNWVTFSGOYNISMR 120
 |||||||
 Db 449 tchmdvfhmaddfsvnitdsgnysgecgstllaesikpappfnvtfisgyniswr 508

QY 121 SDYEDPAFYMLKGLKLOYEYRNKGDPMWVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 |||||||
 Db 509 sdyedpafymkglklyelgyrnrgdpwvsprkllsvdsrsvsllplefrkdsseyelq 568

QY 181 VRAGPMGSSYOGTSEMSDPVIFQOSEELKEGMNPH 218
 |||||||
 Db 569 vragpmpgssyogtsemsdpvifqtqseelkegmnp 606

RESULT 10
 AAY79316
 ID AAY79316 standard; Protein; 606 AA.

XX AAY79316;

DT 18-JUL-2000 (first entry)

DE Maltose binding protein-zalphall fusion protein.

XX Cytokine receptor; zalphall; maltose binding protein; human;
 KW apoptosis; signal transduction; growth factor; cancer; tumour;
 XX Infection; gene therapy; diagnosis; huzalphall/MBP-6H.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..388 "maltose binding protein"

FT Protein 389..606 /note="zalphall cytokine binding domain"

PN WO200017235-A2.

PD 30-MAR-2000.

PF 23-SEP-1999; 99WO-US22149.

XX 23-SEP-1998; 9805-0159254.
 PR 09-MAR-1999; 9905-0265117.
 PR 06-JUL-1999; 9905-0347930.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
 DR WPI: 2000-292825/25.
 DR N-PDB: AA294554.
 XX
 PT Novel nucleic acid encoding zalpahal polypeptide, useful for treating
 PT e.g. viral infection or tumors, and for identifying ligands that
 PT stimulate cell proliferation .
 XX
 PS Example 13; Page 166-168; 190pp; English.

XX The present sequence is that of a fusion protein, designated
 CC huZalpalhal1/MBP-6H, comprising a maltose binding protein (MBP)
 CC fused to the cytokine binding domain (amino acids 20-237) of
 CC human class I cytokine receptor zalpahal1 (see AAY9312). An
 CC expression plasmid containing huZalpalhal1/MBP-6H DNA (see AA294554)
 CC was constructed via homologous recombination and the fusion protein
 CC was expressed in Escherichia coli BL21 using vector plasmid pTAP98.
 CC Zalpalhal1 may be involved in an apoptotic cellular pathway, or is a
 CC cell-cell signaling molecule, growth factor receptor, or
 CC extracellular matrix associated protein with growth factor hormone
 CC activity. The invention provides zalpahal polypeptides (including
 CC fusion proteins), polynucleotides and antibodies, and methods for
 CC their use in the treatment and diagnosis of conditions associated
 CC with altered zalpahal1 expression or activity.
 XX

SO Sequence 606 AA:

Query Match 100.0%; Score 1195; DB 21; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYDLYQTVICILEMNNLHPSTLTLTWDOYEELKDEATSCSLHRSANATHATY 60
 Db 389 cpdlvcydydlyqtvicilemnlhpsltltwqdyeelkdeatscslhrsanathaty 448
 QY 61 TCHMDVHFHMADDFISVNTDOSGNSOEGCSFLAESIKPAPFNVTYFSGOYNISWR 120
 Db 449 tchmdvfhmadddifsvntdsgnsgqcsflaesikpappfnvtvtfsgynlswr 508
 QY 121 SDYEDPAFYMLKGLQYELQYRNRCDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYEQ 180
 Db 509 sdyedpafymkglqyelyrnrgdpwavsprkllsvdsrsvslplefrkdsseyeq 568
 QY 181 VRAGPMGSSYOGTWSKSDPVIFOTOSEELKEGWNPH 218
 Db 569 vragpmpgssyogtwsksdpvifotqseelkegwmpnh 606

RESULT 11

AAAY94304 ID AAY94304 standard; Protein; 538 AA.

AC AAY94304;

XX 08-AUG-2000 (first entry)

DE Human HNOVILR polypeptide 1.

XX Human: anticancer; anti-inflammatory; immunosuppressive; antiallergic;
 KW antiasthmatic; antihemmatic; antiarthritic; nootropic; vasotropic;
 KW neuroprotective; antibacterial; cerebroprotective; osteoprotic;
 KW nephrotropic; hepatotropic; hypotensive; hypertensive; antifungal;
 KW anti-HIV; antiprotozoal; antiviral; antianaemic; autoimmune disease;
 KW Crohn's disease; Alzheimer's disease; Parkinson's disease; stroke;

KW multiple sclerosis; cancer; infection; cardiovascular disease.

XX Homo sapiens.

XX WO200027882-A1.

XX 18-MAY-2000.

XX 01-NOV-1999; 99WO-US25617.

XX 06-NOV-1998; 98US-0187711.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Kikly KR, Michalovich D;

DR WPI: 2000-376497/32.

DR N-PDB: AAA26984.

PT Isolated polypeptide of HNOVILR type used for diagnosing or treating
 PT for example cancer, inflammation, autoimmune disease -

XX Claim 1; Page 30-31; 36pp; English.

XX The present sequence is a HNOVILR polypeptide which is believed to
 CC be a member of the cytokine receptor family of polypeptides. It shows
 CC homology with human interleukin receptor 2 and is therefore expected to
 CC have similar biological functions/properties. The polynucleotide may be
 CC obtained from a cDNA library derived from mRNA in cells of human bone
 CC marrow using expressed sequence tag (EST) analysis. Alternatively it
 CC may be obtained from natural sources such as genomic DNA libraries or
 CC can be synthesised using commercially available techniques. The growth,
 CC regulation and functional activities of cells are regulated through the
 CC interaction of cytokines and their cognate receptors. Thus the
 CC gene sequence and its product are useful for diagnosing or treating a
 CC wide range of diseases including cancer, inflammation, autoimmune
 CC disease, Crohn's disease, allergy, asthma, rheumatoid arthritis,
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis,
 CC head injury damage, septic shock, stroke, osteoporosis, osteoarthritis,
 CC cardiovascular disease, kidney disease, liver disease, ischemic injury,
 CC myocardial infarction, hypotension, hypertension, acquired immune
 CC deficiency syndrome (AIDS), male pattern baldness, and bacterial,
 CC fungal, protozoan and viral infections.
 XX

SO Sequence 538 AA:

Query Match 99.4%; Score 1188; DB 21; Length 538;
 Best Local Similarity 99.5%; Pred. No. 8.5e-115;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPDLVCTDYDLYQTVICILEMNNLHPSTLTLTWDOYEELKDEATSCSLHRSANATHATY 60
 Db 20 cpdlvcydydlyqtvicilemnlhpsltltwqdyeelkdeatscslhrsanathaty 79
 QY 61 TCHMDVHFHMADDFISVNTDOSGNSOEGCSFLAESIKPAPFNVTYFSGOYNISWR 120
 Db 80 tchmdvfhmadddifsvntdsgnsgqcsflaesikpappfnvtvtfsgynlswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRCDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYEQ 180
 Db 140 sdyedpafymkglqyelyrnrgdpwavsprkllsvdsrsvslplefrkdsseyeq 199
 QY 181 VRAGPMGSSYOGTWSKSDPVIFOTOSEELKEGWNPH 218
 Db 200 vragpmpgssyogtwsksdpvifotqseelkegwmpnh 237

RESULT 12

AAU08728 ID AAU08728 standard; Protein; 538 AA.

AC AAU08728;

XX 19-DEC-2001 (first entry)

DE Human HNOVILR polypeptide sequence #1.

XX

KM Human; HNOVILR: cancer; inflammation; rheumatoid arthritis; autoimmunity;
 KM allergy; Crohn's disease; Alzheimer's disease; Parkinson's disease; AIDS;
 KM multiple sclerosis; stroke; sepsis; osteoporosis; ischaemia; hypotension;
 KM myocardial infarction; hypertension; acquired immunodeficiency syndrome;
 KM fungal disease; bacterial disease; viral disease; cytostatic; neutropenic;
 KM anti-inflammatory; immunosuppressive; antiallergic; neuroprotective;
 KM anti-Parkinsonian; cerebrotective; antibacterial; osteoprotic;
 KM vasotropic; cardiac; hypotensive; antihypertensive; anti-HIV; gene therapy;
 KM human immunodeficiency virus; fungicide; antibacterial; virucide.

XX Homo sapiens.

OS

XX US2001025022-A1.

PN

XX 27-SEP-2001.

PD

XX 11-JAN-2001; 2001US-0758664.

PR 26-NOV-1997; 97EP-0309517.

PR 06-NOV-1998; 98US-0187711.

XX

PA (KIKL/) KIKLY K K.

XX (MICH/) MICHALOVICH D.

PI KIKLY KK, Michalovich D;

XX

XX WPI: 2001-638508/73.

DR N-PSDB: AAS14744.

XX

PT New HNOVILR polypeptides and polynucleotides, useful for treating or
 PT diagnosing e.g. cancer, inflammation, autoimmunity, allergy,
 PT Alzheimer's disease, Parkinson's disease, multiple sclerosis, stroke,
 PT osteoporosis or ischaemia -

XX

PS Claim 1; Page 11-12; 17pp; English.

XX

CC The invention relates to human HNOVILR polynucleotides and polypeptides.
 CC The sequences can be used for diagnosing a disease or a susceptibility to
 CC a disease related to expression or activity of the polypeptide by
 CC determining the presence or absence of a mutation in the nucleotide
 CC sequence and/or analysing for the presence or amount of polypeptide
 CC expression in a sample derived from the subject. The HNOVILR polypeptides
 CC and polynucleotides are useful for screening to identify compounds that
 CC stimulate or inhibit the function of the polypeptide. These compounds and
 CC the sequences of the invention can be used for treating or diagnosing
 CC cancer, inflammation (e.g. Rheumatoid arthritis), autoimmunity, allergy,
 CC Crohn's disease, Alzheimer's disease, Parkinson's disease, multiple
 CC sclerosis, stroke, sepsis, osteoporosis, ischaemia, myocardial
 CC infection, hypotension, hypertension, acquired immunodeficiency syndrome
 CC (AIDS), or fungal, bacterial or viral diseases. This sequence represents
 CC an HNOVILR polypeptide.

XX

XX Sequence 538 AA:

SO

Query Match 99.4%; Score 1188; DB 22; Length 538;
 Best Local Similarity 99.5%; Pred. No. 8.5e-115;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CPDLVCYTYLYLTQVLCILMMNMLHPSTLTWTWODYEELKDEATSCSLHRSANHTAHY 60
 |||||||
 DB 20 cpdlvcytylyltqvtcllemnmlhpsltltltwgdqyeelkdeatscslhrrshnathay 79
 |||||||

OY 61 TCHMDVYFHFMAADDIFSVNTDOSGNTSQECGSEFLAESTIKPAPENVVTYFSGQYNISMR 120
 |||||||
 DB 80 tchmdvfhfmaddifsvntldsgnysgcgsfliaesikpappfvtvtfvtsqyniswr 139
 |||||||

OY • 121 SDVEDPAFVWLKGLQYELQYRNRRDPMWAVSPRRKLISVDSNSVSLPLEFFKSDSYELQ 180

DB 140 sdyedpafvmlkklqyqlgrynrgdpmwvpsrrklisvdsnsvslhpleffkdsyeld 199
 |||||||

OY 181 VRAGPMFGSSYQGTWSEWSDPVIFOTOSEELKKGMPH 218
 |||||||

DB 200 vragpmpgssyqgtwsewspdvlftqgseelkegwnph 237
 |||||||

RESULT 13
 AAY45030
 ID AAY45030 standard; Protein; 471 AA.

XX

XX AAY45030;

AC

XX 31-MAY-2000 (first entry)

DT

XX

DE HUMAN OCR10-Fc fusion protein.

XX

XX Human; Orphan Cytokine Receptor-10; OCR10; chromosome 16p12; treatment;
 KM screen; cytokine; cognate ligand; endocrine disorder; immune disorder;
 KM HUMAN OCR10-Fc fusion protein; crystallisable fragment; Fc.

XX

XX Homo sapiens.

OS

XX Synthetic.

OS

XX Key

FT Domain

FT 1..236
 /label= Extracellular_domain
 /note= "Corresponds to HUMAN OCR10"

XX

XX WO200008152-A1.

PN

XX 17-FEB-2000.

PD

XX

XX 16-JUL-1999; 99WO-US16060.

PF

XX 04-AUG-1998; 98US-0128820.

PR

XX (REG-) REGENERON PHARM INC.

PA

XX Maslakowski PJ, Morris J, Valenzuela DM;

PI

XX WPI: 2000-205707/18.

DR N-PSDB: AAZ50747.

XX

XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening
 PT for drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands -

XX

XX Example 6; Page 31-33; 54pp; English.

PS

XX The present sequence is that of HUMAN OCR10-Fc fusion protein, which is
 CC expressed as a soluble secreted protein. It comprises of extracellular
 CC domain from HUMAN OCR10 and crystallisable fragment (Fc) region of human
 CC immunoglobulin gamma-1 (1961). HUMAN OCR10-Fc DNA insert can
 CC be used to transform host cells or for studying efficacy of drugs for
 CC diseases associated with HUMAN OCR10 or OCR10-A polypeptide-mediated
 CC signal transduction. HUMAN Orphan Cytokine Receptor-10 (OCR10) gene is
 CC located on chromosome 16p12. It is expressed at high levels in spleen,
 CC thymus, peripheral blood leucocytes and lymph nodes and moderately in
 CC heart and placenta. It has a role in immune system and cytokine function.
 CC It is useful in screening for cognate ligands or drugs that mediate
 CC survival and differentiation of cells expressing this receptor. Modified
 CC HUMAN OCR10 or its agonist can be used in the treatment of endocrine or
 CC immune disorders.

XX

XX Sequence 471 AA;

SO

Query Match 99.3%; Score 1187; DB 21; Length 471;
 Best Local Similarity 100.0%; Pred. No. 8.9e-115;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYDLYQVTCILEMNNLHPSTLTITWODYELKDEATSCSLHRSANATHARY 60
 DB 20 cpdlvctdydlyqvtvcllemnnlhpsltltitwqdyeelkdeatscslhrsanathary 79
 QY 61 TCHMDVFEHMADDFSVNITDQSGNYSOEGCSFLLASIRKPPFPNTVTFSCQYNIWR 120
 DB 80 tchmdvfhmaddfsvnltqsgnyseegcsfllaesirppfpntvtfsgqynlswr 139
 QY 121 SDYEDPAFYMLGKLOLEYLQYRNRCDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180
 DB 140 sdyedpafymlgklyqlyeyrnrgdpwavsprkrlisvdsrsvsllplefrkdsseylq 199
 QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTOSEELKEGMNP 217
 DB 200 vragpmpgssyqgtwsewdpvlftqgseelkegmnp 236

SUPL 14
 ID AE02459 standard; Protein: 538 AA.
 AC AAE02459;
 XX 10-AUG-2001 (first entry)
 DE Human DNA cytokine receptor subunit 3.2 (DCRS3.2).
 XX Human; immunomodulator; DNA cytokine receptor subunit 3.2; DCRS3.2;
 KM therapy; immunological disorder; drug screening; cell development;
 XX chromosome 16p12; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Signal_peptide 21..538
 FT /label= DCRS3.2
 FT /note= "Human mature DNA cytokine receptor subunit 3.2"
 FT Misc-difference 108
 FT /note= "Encoded by GAN"
 FT Misc-difference 136
 FT /note= "Encoded by ATN"
 FT Misc-difference 199
 FT /note= "Encoded by CAN"

MO200136467-A2.
 XX 25-MAY-2001.
 PD 16-NOV-2000; 2000MO-US31363.
 PF 18-NOV-1999; 99US-0443060.
 PR 13-DEC-1999; 99US-0170320.
 XX (SCHE) SCHERING CORP.
 PA Gorman DM;
 XX PI
 DR WPI, 2001-343800/36.
 DR N-PSDB; AAD06412.
 XX New mammalian receptor proteins related to cytokine receptors, useful
 PT for regulating cell development and for diagnosis and treatment of
 PT immunological disorders -
 XX Claim 3; Page 16-17; 124pp; English.
 XX The present sequence is human DNA cytokine receptor subunit 3.2
 CC (DCRS3.2) cDNA. DCRS3 gene is located on chromosome 16p12.
 CC Cytokine receptors, fragments and antibodies are useful for treating

CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
 CC useful in drug screening to identify compounds having binding affinity
 CC to the receptor subunit. Modulators of DCRs are useful for modulating
 CC the physiology or development of a cell or tissue culture cells. A
 CC purified DCRS is useful as a reagent to detect antibodies generated in
 CC response to the presence of elevated levels of expression, or
 CC immunological disorders which lead to production of antibody to the
 CC endogenous receptor. Cytokine receptor sequences are useful as probes
 CC for detecting levels of the cytokine receptor in patients suspected of
 CC having an immunological disorder. Antibodies have therapeutic value, are
 CC useful as potent antagonists, in detecting or quantifying ligands, for
 CC isolating DCRs proteins and peptides, to screen expression libraries for
 CC particular expression products, to raise anti-idiotypic antibodies and
 CC for detecting or diagnosing various immunological conditions related to
 CC expression of the protein or cells which express the protein.

SQ Sequence 538 AA:
 QY 1 CPDLVCTDYDLYQVTCILEMNNLHPSTLTITWODYELKDEATSCSLHRSANATHARY 60
 DB 20 cpdlvctdydlyqvtvcllemnnlhpsltltitwqdyeelkdeatscslhrsanathary 79
 QY 61 TCHMDVFEHMADDFSVNITDQSGNYSOEGCSFLLASIRKPPFPNTVTFSCQYNIWR 120
 DB 80 tchmdvfhmaddfsvnltqsgnyseegcsfllaesirppfpntvtfsgqynlswr 139
 QY 121 SDYEDPAFYMLGKLOLEYLQYRNRCDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180
 DB 140 sdyedpafymlgklyqlyeyrnrgdpwavsprkrlisvdsrsvsllplefrkdsseylq 199
 QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTOSEELKEGMNP 218
 DB 200 vragpmpgssyqgtwsewdpvlftqgseelkegmnp 237

RESULT 15
 AAY69888
 ID AAY69888 standard; Protein: 538 AA.
 XX AAY69888;
 AC AAY69888;
 XX 24-MAY-2000 (first entry)
 DE Mouse haemopoietin receptor family member NR8gamma.
 XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KM blood formation disorder.
 XX Mus sp.
 OS WO9967290-A1.
 PN 29-DEC-1999.
 PD 23-JUN-1999; 99WO-UP03351.
 PF 24-JUN-1998; 98JP-0214720.
 PR 19-OCT-1998; 98JP-0297409.
 XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 PA Nomura H, Maeda M;
 XX PI
 DR WPI, 2000-116933/10.
 DR N-PSDB; AAZ59242.
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -

XX Claim 6; Page 152-158; 176pp; Japanese.
 PS
 CC This sequence represents a mouse haemopoietin receptor protein family
 CC NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used
 CC for the diagnosis of blood formation disorders. Compounds identified as
 CC binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 538 AA;

Query Match 97.0%; Score 1159; DB 21; Length 538;
 Best Local Similarity 98.2%; Pred. No. 8.8e-112;
 Matches 214; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CPDLVYTYDTYLTCTCTLEMMNLHPSRTLTWDOYFELEKDEATSCSLHRSANATHATY 60
 Db 20 CPDLVYTYDTYLTCTCTLEMMNLHPSRTLTWDOYFELEKDEATSCSLHRSANATHATY 79
 QY 61 TCHMDVYFHFMAADDIFSVNITDQSGNYSQEGSFLAESIKRPAPFNVTVTFSGOYNISWR 120
 80 TCHMDVYFHFMAADDIFSVNITDQSGNYSQEGSFLAESIKRPAPFNVTVTFSGOYNISWR 139
 QY 121 SDVEDPAFYWLKGLQYELQYRNRCDPWAVSPRKLSVDSRSYSLPLEFRKSSYEIQ 180
 Db 140 SDVEDPAFYWLKGLQYELQYRNRCDPWAVSPRKLSVDSRSYSLPLEFRKSSYEIQ 199
 QY 181 VRAGPMGSSSYOGTSEMSDPIVTFQTOSEELKEGMNPH 218
 Db 200 VRAGPMGSSSYOGTSEMSDPIVTFQTOSEELKEGMNPH 237

Search completed: June 28, 2002, 07:46:28
 Job time: 343 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2002, 07:46:28 ; Search time 110.69 Seconds
(without alignments)
162.562 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850
Sequence: 1 MRSSPCNMERIVICLMVIFL.....LLQKMIHQHLSRTHGSDS 162

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*

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13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*

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21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	21	AA18623
2	695.5	81.8	519	21	AA18627
3	486	57.2	146	21	AA18624
4	394	46.4	510	21	AA18628
5	212	24.9	40	21	AA18625
6	176	20.7	32	21	AA18626
7	103.5	12.2	133	21	AA18625
8	99.5	11.7	114	16	AA18625
9	99.5	11.7	114	16	AA18625
10	99.5	11.7	114	16	AA18625
11	99.5	11.7	114	17	AA18625

12	99.5	11.7	114	17	AA18625	Generic mammalian
13	99.5	11.7	114	19	AA18625	Simian epithelium
14	99.5	11.7	114	20	AA18625	Simian epithelium
15	99.5	11.7	114	21	AA18625	Mature simian epit
16	99.5	11.7	114	22	AA18625	Simian ERF (SETF)
17	99.5	11.7	162	16	AA18625	Human interleukin-
18	99.5	11.7	162	16	AA18625	Human IL-15. Homo
19	99.5	11.7	162	17	AA18625	Simian epithelium
20	99.5	11.7	162	17	AA18625	Human epithelium-d
21	99.5	11.7	162	17	AA18625	Human interleukin-
22	99.5	11.7	162	18	AA18625	Wild-type interlu
23	99.5	11.7	162	18	AA18625	Human interleukin-
24	99.5	11.7	162	19	AA18625	Human interleukin-
25	99.5	11.7	162	19	AA18625	Simian epithelium
26	99.5	11.7	162	20	AA18625	Simian epithelium
27	99.5	11.7	162	21	AA18625	Amino acid sequenc
28	99.5	11.7	162	21	AA18625	Human interleukin-
29	99.5	11.7	162	21	AA18625	Human interleukin-
30	99.5	11.7	162	22	AA18625	Human interleukin-
31	99.5	11.7	162	22	AA18625	Simian ERF (SETF)
32	99.5	11.7	162	22	AA18625	Human interleukin-
33	99.5	11.7	162	22	AA18625	Human IL-15. Homo
34	99.5	11.7	114	16	AA18625	Simian interleukin
35	99.5	11.7	114	17	AA18625	Human mature epith
36	99.5	11.7	114	19	AA18625	Human epithelium d
37	99.5	11.7	114	20	AA18625	Human epithelium-d
38	99.5	11.7	114	21	AA18625	Mature human epith
39	99.5	11.7	114	22	AA18625	Human ERF (SETF) m
40	99.5	11.7	122	17	AA18625	Recombinant flag s
41	99.5	11.7	162	16	AA18625	Simian interleukin
42	99.5	11.7	162	16	AA18625	Simian IL-15. Cer
43	99.5	11.7	162	17	AA18625	Human epithelium d
44	99.5	11.7	162	17	AA18625	Simian epithelium-
45	99.5	11.7	162	17	AA18625	Simian interleukin

ALIGNMENTS

RESULT	1
ID	AA18623
AC	AA18623 standard; Protein: 162 AA.
XX	
XX	AA18623;
DT	22-JAN-2001 (first entry)
DE	
XX	A human zalphal1 ligand polypeptide.
XX	
KW	zalphal1 ligand; cytokine; haematopoietic cell proliferation; lymphoma
KW	tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
XX	
OS	Homo sapiens.
XX	
PN	WO200053761-A2.
XX	
PD	14-SEP-2000.
XX	
PF	09-MAR-2000; 2000WO-US06067.
XX	
PR	09-MAR-1999; 99US-0264908.
PR	11-MAR-1999; 99US-0265992.
PR	01-JUL-1999; 99US-0142013.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI	Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX	
DR	WPI: 2000-565600/52.
XX	
DR	N-PSDB: AAA75552.
XX	
PT	New human cytokine, designated zalphal1 ligand, useful for stimulating

XX	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI	Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX	WPI: 2000-565600/52.
DR	N-PSDB: AAA75580.
XX	
PT	New human cytokine, designated zalphall ligand, useful for stimulating
PT	the proliferation and/or development of haematopoietic cells in vitro
PT	and in vivo, and for treating tumourigenesis -
XX	
PS	Disclosure: Page 222-223; 256pp; English.
XX	
CC	The present sequence represents a mouse zalphall ligand polypeptide,
CC	which is a cytokine. The zalphall ligand is useful for stimulating the
CC	proliferation and development of haematopoietic cells in vitro and in
CC	vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC	for cloning the zalphall gene. The zalphall ligand is useful for
CC	treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be
CC	used for treating leukemias and lymphomas. Antagonists against zalphall
CC	ligand are useful as research reagents for characterizing ligand-receptor
CC	interaction. Antagonists are also useful for inhibiting expansion,
CC	proliferation, activation and differentiation of cells involved in
CC	regulating hematopoiesis. The zalphall ligand may also be used to
CC	stimulate an immune response against B cell tumour, a virus, a parasite
CC	or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC	agonists and antibodies are also useful for the detection, diagnosis,
CC	prevention, and treatment of diseases associated with a zalphall ligand
CC	genetic defect.
XX	
SO	Sequence 146 AA;
XX	
Query Match	57.2%; Score 486; DB 21; Length 146;
Best Local Similarity	63.0%; Pred. NO. 2.4e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;	
OY	8 MERIVICLVIFLGLTVHKSSQSGODRHMRKQLIDIVDQIKNYVNDLVPEFLPAPEDV 67
DB	1 MERTVICLVIFLGLTVHKKSSQSGODRHMRKQLIDIVDQIKNYVNDLVPEFLPAPEDV 60
OY	68 EFNCEWSAFSCQKAKQKLSANTGNNERILNVSIRKLRKRPSTNAGRQKRLTQPCSDS 127
DB	61 KYNCEHAFAIACQKAKLRPSNPNKLTFLIDVAGLITRRIPATRGKKQKXKLNKACPSGDS 120
OY	128 YEKKRPELEERFKSLQKMIHOHS 153
DB	121 YEKTRPELEERFKSLQKMIHOHS 146
RESULT 4	
AAB18628	
ID	AAB18628 standard; Protein; 510 AA.
XX	
CC	AAB18628;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of MBP-mouse zalphall ligand fusion in pTAP134.
XX	
KW	zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW	tumourigenesis; leukaemia; hematopoiesis; B cell tumour.
OS	Synthetic.
OS	Mus musculus.
XX	
XX	MO200053761-A2.
PN	
PD	14-SEP-2000.
XX	
PF	09-MAR-2000; 2000MO-US06067.
XX	
PR	09-MAR-1999; 99US-0264908.

PR	11-MAR-1999;	99US-0265992.
PR	01-JUL-1999;	99US-0142013.
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA,	
PI	Johnston JV, Nelson AJ, Dillon SR, Hammond AK;	
XX		
DR	WPI: 2000-565600/52.	
XX	N-PSDB; AAA75602.	
PT	New human cytokine, designated zalphall ligand, useful for stimulating	
PT	the proliferation and/or development of haematopoietic cells in vitro	
PT	and in vivo, and for treating tumourigenesis -	
XX		
XX	Example 31; Page 239-240; 256pp; English.	
XX		
CC	The present sequence represents a MBP-mouse zalphall ligand fusion in	
CC	the plasmid pTAP126. zalphall ligand is a cytokine. The zalphall ligand	
CC	is useful for stimulating the proliferation and development of	
CC	haematopoietic cells in vitro and in vivo. Zalphall ligand	
CC	polynucleotides can be used as primers or probes for cloning the	
CC	zalphall gene. The zalphall ligand is useful for treating tumourigenesis.	
CC	A zalphall ligand-saporin fusion toxin may be used for treating	
CC	leukaemias and lymphomas. Antagonists against zalphall ligand are	
CC	useful as research reagents for characterizing ligand-receptor	
CC	interaction. Antagonists are also useful for inhibiting expansion,	
CC	proliferation, activation and differentiation of cells involved in	
CC	regulating haematopoiesis. The zalphall ligand may also be used to	
CC	stimulate an immune response against B cell tumour, a virus, a parasite	
CC	or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,	
CC	agonists and antibodies are also useful for the detection, diagnosis,	
CC	prevention, and treatment of diseases associated with a zalphall ligand	
CC	genetic defect.	
XX		
XX	Sequence 510 AA;	
XX		
Query Match	46.4%; Score 394; DB 21; Length 510;	
Best Local Similarity	62.0%; Pred. No. 2.5e-35;	
Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;		
Oy	33 DRHMRQLIDVDOLKANYNDLVPEDLVPEDEVTCNEMSAFSCFOKAOLKSANTGNN 92	
Db	390 dtrllrrlhlldiveqlklyendipellsapqgvkgncehaafacfgkaklkpsnpgn 449	
Oy	93 ERTINWSIKKLKRKRPRSTNAGRKQKHNRLTSPSCDSYEKKRPREFLERKSLLOKNIHNL 152	
Db	450 ktfildlvaqrrlrtparrgkqkqhiakcpcscdsyekrtepfierlkwllqkmbhql 509	
Oy	153 s 153	
Db	510 s 510	
RESULT 5		
ID	AAAB18625	
XX	AAAB18625 standard; Peptide; 40 AA.	
XX	AAAB18625;	
XX		
DT	22-JAN-2001 (first entry)	
XX		
DE	Antigenic peptide derived from a human zalphall ligand polypeptide.	
XX		
XX	zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;	
KW	tumourigenesis; leukaemia; hematopoiesis; B cell tumour.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200053761-A2.	
XX		
DD	14-SEP-2000.	

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XX 09-MAR-2000; 200OWO-US06067.
PE
XX 09-MAR-1999; 99US-0264908.
PR 11-MAR-1999; 99US-0265992.
XX 01-JUL-1999; 99US-0142013.
PA
XX (ZYMO ) ZYMOGENETICS INC.
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnson JV, Nelson AJ, Dillon SR, Hammond AK;
DR WPI: 2000-565600/52.
XX
XX New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
PT and in vivo, and for treating tumourigenesis -
XX
XX Example 34; Page 227: 256pp; English.
XX
XX The present sequence was used to raise antibodies, and is derived from
CC a human zalphall ligand polypeptide. Zalphall ligand is a cytokine.
CC The zalphall ligand is useful for stimulating the proliferation and
CC development of haematopoietic cells in vitro and in vivo. Zalphall
CC ligand polynucleotides can be used as primers or probes for cloning the
CC zalphall gene. The zalphall ligand is useful for treating tumourigenesis.
CC A zalphall ligand-saporin fusion toxin may be used for treating
CC leukaemias and lymphomas. Antagonists against zalphall ligand are
CC useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect.
XX
XX Sequence 40 AA.
SO

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XX 01-JUL-1999;      99US-0142013.
PA (ZYMO ) ZYMOGENETICS INC.
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AU, Dillon SR, Hammond AK;
DR WPI; 2000-565600/52.
XX
PT New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
PT and in vivo, and for treating tumourigenesis -
XX
PS Example 34; Page 227; 256pp; English.
XX
CC The present sequence was used to raise antibodies, and is derived from
CC a human zalphall ligand polypeptide. Zalphall ligand is a cytokine.
CC The zalphall ligand is useful for stimulating the proliferation and
CC development of haematopoietic cells in vitro and in vivo. Zalphall
CC ligand polynucleotides can be used as primers or probes for cloning the
CC zalphall gene. The zalphall ligand is useful for treating tumourigenesis.
CC A zalphall ligand-saporin fusion toxin may be used for treating
CC leukaemias and lymphomas. Antagonists against zalphall ligand are
CC useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect.
XX
SQ Sequence      32 AA;
OY Query Match          20.7%; Score 176; DB 21; Length 32;
Db   Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
    Matches 32; Conservative 0; Pident No. 1.6e-12;
    122 CPSCDSYEKKPKPEFLERFKSLQKMIHOHLS 153
       |||||||
    Db 1 cpscdsyekpkpeflerfkstllqmbqhpls 32
RESULT_7
AAV54825
ID AAV54825 standard; Protein; 135 AA.
AC AAV54825;
DT 04-FEB-2000 (first entry)
DE Human Interleukin-15 protein sequence.
KW Interleukin-15; IL-15; antisense inhibitor; untranslated region; 5'UTR;
OS Homo sapiens.
PN US5985663-A.
PD 16-NOV-1999.
PF 25-NOV-1998; 98US-0200141.
PR 25-NOV-1998; 98US-0200141.
PA (ISIS-) ISIS PHARM INC.
PI Bennett CF, Cowser LM;
WPI; 2000-022283/02.

```


XX PS Claim 1; Page 33; 48pp; English.
 CC A simian species of IL-15 (sIL-15) was purified and its AA
 CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
 CC AAR00524, AAR00525). Both the simian and the human ORFs encode
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor
 CC polypeptides each comprise a 48-AA leader sequence and a sequence
 CC encoding mature simian or human IL-15 polypeptides. The active
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
 CC AAR83310 respectively. The invention also comprises other mammalian
 CC IL-15, including human IL-15, that hybridise to probes defined by
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
 CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
 CC The deposit was named 141-HERF. AAR83435 is a mammalian mature
 CC IL-15 polypeptide. It is a generic sequence which encompasses both
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
 XX SQ Sequence 114 AA;

Query Match 11.7%; Score 99.5; DB 16; Length 114;
 Best Local Similarity 25.2%; Pred. No. 0.0031;
 Matches 30; Conservative 23; Mismatches 45; Indels 21; Gaps 5;
 QY 43 IDIVDQKKNVNDLVEPF-----LPAPEDVETNCESAFSCF-QKAQLKSANTGNN---- 92
 Db 3 vnvtsdlkk-iedlqsmhidatlyesdvhpckvtankcfllelqvysxesgxxihd 61
 QY 93 --ERINVSIRKLRKPPSTNAGRQKHRLTGPCSDSYEKRPKEFLERFKSLQKMH 149
 Db 62 tvenllllannxllsngnxtesg-----ckeceeleekniketlqsfvhiygmfin 112

RESULT 10
 AAR66928
 ID AAR66928 standard; Protein; 114 AA.
 XX AC AAR66928;
 XX DT 04-SEP-1995 (first entry)
 XX DE Mammalian IL-15.
 XX KM Interleukin-15, IL-15; sIL-15; T-cell growth factor;
 XX KW antitumor; vifrucide.
 XX OS Mammalia.
 XX Key Location/Qualifiers
 FT MISC-difference 52 /label= Leu, His
 FT MISC-difference 57 /label= Ala, Thr
 FT MISC-difference 58 /label= Ser, Asp
 FT MISC-difference 73 /label= Ser, Ile
 FT MISC-difference 80 /label= Val, Ile
 XX FT
 XX PN ZA9402636-A.
 XX PD 28-DEC-1994.
 XX PF 18-APR-1994; 94ZA-0002636.
 XX PR 18-APR-1994; 94ZA-0002636.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 XX PI Rauch C;

XX DR WPI; 1995-082473/11.
 XX PT New purified interleukin-15 - which induces T cell proliferation
 XX PT and differentiation, used for the treatment of tumours and viral
 XX PT infection
 XX PS Claim 1; Page 33; 47pp; English.
 CC A simian and human IL-15 cDNAs (AA084583-84) can be used to obtain
 CC cDNAs encoding other mammalian homologs of IL-15. A general
 CC sequence of mammalian IL-15 is claimed.
 XX SQ Sequence 114 AA;

Query Match 11.7%; Score 99.5; DB 16; Length 114;
 Best Local Similarity 25.2%; Pred. No. 0.0031;
 Matches 30; Conservative 23; Mismatches 45; Indels 21; Gaps 5;
 QY 43 IDIVDQKKNVNDLVEPF-----LPAPEDVETNCESAFSCF-QKAQLKSANTGNN---- 92
 Db 3 vnvtsdlkk-iedlqsmhidatlyesdvhpckvtankcfllelqvysxesgxxihd 61
 QY 93 --ERINVSIRKLRKPPSTNAGRQKHRLTGPCSDSYEKRPKEFLERFKSLQKMH 149
 Db 62 tvenllllannxllsngnxtesg-----ckeceeleekniketlqsfvhiygmfin 112

RESULT 11
 AAW09099
 ID AAW09099 standard; Protein; 114 AA.
 XX AC AAW09099;
 XX DT 11-MAR-1997 (first entry)
 XX DE Simian mature epithelium derived T cell factor.
 XX KM sEPF; African green monkey; CV1/EBNA cell; T-cell; B-cell;
 XX KW lymphocyte; proliferation; differentiation; gastrointestinal;
 XX KW HIV infection; human immunodeficiency virus.
 XX OS Cercopithecus aethiops.
 XX Key Location/Qualifiers
 FT MISC-difference 1.114
 FT MISC-difference 1.114 /label= mature_sEPF
 XX FT
 XX PN US5574138-A.
 XX PD 12-NOV-1996.
 XX PF 08-MAR-1993; 93US-0031399.
 XX PR 22-FEB-1995; 95US-0393305.
 XX PR 08-MAR-1993; 93US-0031399.
 XX PR 22-APR-1994; 94US-0233606.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 XX PI Rauch C;
 XX DR WPI; 1996-517923/51.
 XX DR N-PDB; AAT94955.
 XX PT New epithelium derived T cell factor - induces proliferation of T
 XX PT and B cells; stimulates destruction of tumour and virus-infected
 XX PT cells and protects against toxicity, partic. for treating intestinal
 XX PT disease and HIV infection
 XX PS Claim 1; Fig 1; 35pp; English.

	Only Match	11.7%	Score 99.5	DB 17,	Length 114;
	Best Local Similarity	25.2%	Pred No. 0.0031;		
	Matches	30;	Conservative	23;	Mismatches 45; Indels 21; Gaps 5
QY	43 IDIYDQKNTVNDLYPEF-----LPAPDEVELNCEMSAFSCF-QKAQLKSANTGN--	----	92		
Dd	3 vvvvstdkl-iedlgshmdatilyesdvhpscvtmckcllelqysksesdxixhd	61			
QY	93 --EELINVSIIKKLRKPSTNAGRGRHRLPCSDSYEKRPKEFLERFSKLQMKIH	149			
Dd	62 tvevlllllaamxissngnxsyesg-----skceeeelxxmkieffgsyfiavgmfin	112			

XX	RESULT_13	
XX	ID	AAW39186
XX	AAW39186	standard; Protein; 114 AA.
XX	AC	AAW39186;
XX	DT	08-MAY-1998 (first entry)
XX	DE	Simian epithelium derived T-cell factor mature protein.
XX	KW	Epithelium derived T-cell factor; ETF; Simian; gastrointestinal disease
XX	KW	B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
XX	OS	Simian.
XX	Key	Location/Qualifiers
XX	FT	1..114
XX	FT	/label= ETF
XX	PN	US5707616-A.
XX	PD	13-JAN-1998.
XX	PF	04-OCT-1996; 96US-0726817.
XX	PR	22-FEB-1995; 95US-0393305.
XX	PR	08-MAR-1993; 93US-0031399.
XX	PA	22-APR-1994; 94US-0233606.
XX	PA	(IMMV) IMMUNEX CORP.
XX	P1	Anderson DM, Eisenman JR, Fung V, Grabstein KH;
XX	P1	Rauch C;
XX	DR	WPI: 1998-100295/09.
XX	DR	N-PSDB; AAW02873.
XX	FT	Treatment or prevention of gastrointestinal diseases - by
XX	PS	administering epithelium-derived T-cell factor polypeptide
XX	PS	Claim 1a: Column 37-38; 34pp; English.
XX	CC	This sequence represents a simian epithelium-derived T-cell factor (ETF)

CC The invention relates to an isolated antibody that binds specifically to
CC a simian or human epithelium-derived T-cell factor (EUF) polypeptide. Rh
CC antibodies are used, optionally when immobilized or labeled, to detect
CC and quantify EUF in standard immunoassays. They may also be used as
CC diagnostic and therapeutic agents e.g. when conjugated to toxins (or

PT Stimulation of T-cells in human immunodeficiency virus infected
 XX patients -
 PS Claim 1; Fig 1, 33pp; English.
 XX

CC This sequence represents mature simian epithelium-derived T-cell factor
 CC (ETF). This is a previously unidentified T-cell growth factor which
 CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate
 CC and differentiate. It also promotes proliferation of the gastrointestinal
 CC epithelium. The protein can be used to promote long-term in vitro culture
 CC of T-lymphocytes and T-cell lines. ETF can be used for treating HIV
 CC infection, HIV-associated diseases, and other diseases or conditions
 CC where stimulation of T-cell proliferation would be desirable e.g., it
 CC could be used to augment the destruction of tumour cells or virally-
 CC infected cells. ETF may also be used to treat or prevent gastrointestinal
 CC disease, including chemotherapy and radiotherapy associated enteritis,
 CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic
 CC disorders. Chemotherapy and radiotherapy associated enteritis (gut
 CC toxicity) results in bleeding and sepsis due to gastrointestinal flora
 CC entering the blood, and thus can limit the dosage of therapeutic agent
 CC administered to a cancer patient. ETF may therefore be used to increase
 CC the tolerated doses radiotherapy and chemotherapy.

Sequence 114 AA;

Query Match 11.7%; Score 99.5; DB 21; Length 114;
 Best Local Similarity 25.9%; Pred. No. 0.0031;
 Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVDOKNVNDLVPF-----LPAPDYVENCESAFSCF---QKQIKSANTGNNE 93
 Db 3 vnvysdlkx-iedlqgmhdatlyesdvhpckvltamkcfllqlqvistlesgdasind 61
 OY 94 RIINVSIRKLRRKPSTNAGRQKRLTCPCDSYEKKPPKFELEERFKSLQKMH 149
 Db 62 tvenlll--lannslnsgnvtes--gckeceeleeknikelfqsfvnhvqmfan 112

Search completed: June 28, 2002, 07:46:29
 Job time: 344 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:44:32 ; Search time 63.41 seconds
(without alignments)
441.968 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

Sequence: 1 MRSSPGNMERIVICLAWIFL.....LLQKMIHQHLSRTHGSEDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_prodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvirus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	850	100.0	162	4	Q9HBE4	Q9HBE4 homo sapien
2	486	57.2	146	11	Q9ES17	Q9ES17 mus musculu
3	91.5	10.8	367	11	Q05208	Q05208 mus musculu
4	83.5	9.8	3052	12	Q82933	Q82933 johnsongras
5	83	9.8	899	2	Q9R2J7	Q9R2J7 shigella so
6	83	9.8	899	2	Q52336	Q52336 salmonella
7	81.5	9.6	566	5	Q9VVE8	Q9VVE8 dicystostell
8	81	9.5	163	5	Q966R0	Q966R0 dicystostell
9	81	9.5	385	5	Q9VUL7	Q9VUL7 drosophila
10	79.5	9.4	187	13	Q9NK60	Q9NK60 drosophila
11	79.5	9.4	1006	11	Q9W756	Q9W756 gallus galli
12	79.5	9.4	1006	11	Q91Y09	Q91Y09 mus musculu
13	78	9.2	305	11	Q9J148	Q9J148 mus musculu
14	77	9.1	319	4	Q96L14	Q96L14 homo sapien
15	76.5	9.0	421	5	Q9VY89	Q9VY89 drosophila
16	76.5	9.0	424	5	Q23239	Q23239 calliphora

17	75.5	8.9	187	13	Q9DEV5	Q9DEV5 gallus galli
18	75.5	8.9	216	6	Q9BER3	Q9BER3 didelphis m
19	75.5	8.9	336	11	Q62612	Q62612 ratius norv
20	75.5	8.9	406	5	Q22975	Q22975 caenorhabdi
21	75.5	8.9	566	11	Q62611	Q62611 ratius norv
22	75	8.8	357	4	Q96C15	Q96C15 homo sapien
23	74.5	8.8	286	16	Q9P5Y5	Q9P5Y5 ureaplasma
24	74.5	8.8	441	10	Q9C5F0	Q9C5F0 arabidopsis
25	74.5	8.8	484	6	Q9MZ13	Q9MZ13 bos taurus
26	74.5	8.8	848	4	Q75141	Q75141 homo sapien
27	74.5	8.8	1066	10	Q9AV01	Q9AV01 oryza sativ
28	74	8.7	143	13	Q91AC7	Q91AC7 meleagris g
29	74	8.7	201	4	Q9H6V1	Q9H6V1 homo sapien
30	74	8.7	440	10	Q9M2E9	Q9M2E9 arabidopsis
31	74	8.7	457	11	Q9CXV7	Q9CXV7 mus musculu
32	74	8.7	599	12	Q71211	Q71211 grapevine 1
33	74	8.7	599	12	Q39854	Q39854 grapevine 1
34	74	8.7	953	11	Q60442	Q60442 ricecetus
35	74	8.7	2197	5	Q96296	Q96296 plasmodium
36	73.5	8.6	545	5	Q9W3H8	Q9W3H8 chironomus
37	73.5	8.6	545	5	Q9W3H8	Q9W3H8 chironomus
38	73.5	8.6	565	16	Q9V099	Q9V099 staphylococ
39	73.5	8.6	629	8	Q9T708	Q9T708 ginkgo bilo
40	73.5	8.6	770	5	Q44014	Q44014 leishmania
41	73.5	8.6	868	5	Q9NAB8	Q9NAB8 caenorhabdi
42	73.5	8.6	2118	5	Q76904	Q76904 drosophila
43	73.5	8.6	2328	5	Q9VMA7	Q9VMA7 drosophila
44	73.5	8.6	2531	5	Q9CPH4	Q9CPH4 drosophila
45	73	8.6	556	5	Q18181	Q18181 caenorhabdi

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	162 AA.
Q9HBE4	Q9HBE4			
AC	Q9HBE4			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	INTERLEUKIN 21.			
GN	IL21.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20531754; PubMed=11081504;			
RA	Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,			
RA	Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,			
RA	Burkhead S., Heipel M., Brandt C., Kuljper J.L., Kramer J.,			
RA	Conklin D., Presnell S.R., Berry J., Shota F., Bort S., Hamby K.,			
RA	Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,			
RA	Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,			
RA	Maurer M., Kauschansky K., Holly R.D., Foster D.;			
RT	"interleukin 21 and its receptor are involved in NK cell expansion and			
RT	regulation of lymphocyte function.";			
RL	Nature 408:57-63(2000).			
DR	EMBL; AF254069; AAG29348.1; -			
SO	SEQUENCE 162 AA; 18652 MW; 54EPD4EED3AB97FE CRC64;			

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRSSPGNMERIVICLAWIFLGLVHKSSSGODRHMIRMRQLDIYDQKNTVNDLVEEF 60
DB	1	MRSSPGNMERIVICLAWIFLGLVHKSSSGODRHMIRMRQLDIYDQKNTVNDLVEEF 60
QY	61	LPAPDEVETNCWMSAFSCFOKAQLKSANTGNMERIINVSIRKLRKRPSTNAGRRQKRL 120


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DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001436; Peptidase_C6.
DR InterPro: IPR001592; Poly-coat.
DR InterPro: IPR002540; Poly_P1.
DR InterPro: IPR001205; RNA_pol_P3D.
DR Pfam: PF002270; DEAD. 1.
DR Pfam: PF00271; helicase_C. 1.
DR Pfam: PF00863; Peptidase_C4. 1.
DR Pfam: PF00881; Peptidase_C6. 1.
DR Pfam: PF00767; Poly-coat. 1.
DR Pfam: PF01577; Poly_P1. 1.
DR Pfam: PF00680; RNA_dep_RNA_pol. 1.
DR PRINTS: PR00966; NTPOTPTASE.
DR SMART: SM00487; DEXDC. 1.
DR SMART: SM00490; HELICC. 1.
DR ATP-binding: Helicase.
KM CHAIN 239 699 HELPER COMPONENT (HC).
FT CHAIN 700 1046 PROTEASE3.
FT CHAIN 1047 1098 6K1.
FT CHAIN 1099 1757 CYTOPLASMIC INCLUSION (CI).
FT CHAIN 1758 1803 6K2.
FT CHAIN 1804 1991 SMALL NUCLEAR INCLUSION/VIRUS ATTACHED
FT CHAIN 1992 2233 PROTEIN.
FT CHAIN 2234 2749 SMALL NUCLEAR INCLUSION/PROTEASE.
FT CHAIN 2750 3052 LARGE NUCLEAR INCLUSION/POLYMERASE.
FT CHAIN 3052 347247 COAT PROTEIN.
SQ SEQUENCE 3052 AA; 347247 MW; 08CD8831A73EBCA9 CRC64;

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Query Match 9.8%; Score 83.5; DB 12; Length 3052;
Best Local Similarity 23.1%; Pred. No. 21;
Matches 25; Conservative 23; Mismatches 57; Indels 3; Gaps 3;

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OY 45 IYDQKNTVNDLVPEFLPAPEDVETNCMSAFSCFOKAQKSNKNGNRIINVSIRKLK 104
DB 220 LVNALDOYEED-VKQICHSFDEARAFMKFTENHTAQRRHSDHTNEPV-MSVEECG 277
OY 105 RKPESTNAGRQKHRLTQPCSC-DSEYKPKPEFLERFKSLQKMIHQH 151
DB 278 RRAAMLENAFHQGFRTCKHCFQTFDEHSDSEVCERIHNAQRIEQRN 325

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RESULT 5
OYR2J7 PRELIMINARY; PRT; 899 AA.
AC OYR2J7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
RT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE RELAXASE.
GN NIKB.
OS Shigella sonnei.
OG Plasmid Colid-P9.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=624;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P9.
RA Sampei G.; Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete
RT nucleotide sequence of the Colid-P9 genome."
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021078; BAA75140.1; -.
KM Plasmid.
SO SEQUENCE 899 AA; 103977 MW; E7DB0164C54914E3 CRC64;

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Query Match 9.8%; Score 83; DB 2; Length 899;
Best Local Similarity 22.5%; Pred. No. 5.8;
Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;
OY 27 SSSGQODRHMTIMRLIDYDQKNTVNDLVPEFLPAPEDVETNCMSAF---SCFOKAQ 83

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DB 38 SSSQAEQPHRSFSLVDYATRLN-----ESTVALVDMKGGCMVWFYGVTCFHNCT 91
OY 84 LKSANTGNERRIINVSIRKIRKPPSTNAGROKRL---TCP-----SCSYEKRPK 134
DB 92 SLETAADMEVY-----ARQAHYAKDDTDFVFHYILISWOSHESPRPE 133
OY 135 EFLERFKSLQKM---IHQHLSSRTGSEDS 162
DB 134 QYIDSVRHTKSLGLADHQVYA-VHIDTDN 163

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RESULT 6
OY2336 PRELIMINARY; PRT; 899 AA.
AC OY2336;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE NIKB PROTEIN.
GN NIKB.
OS Salmonella typhimurium.
OG Plasmid R64.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Salmonella.
RN NCBI_TaxID=602;
RP [1]
RP SEQUENCE OF 895-899 FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=96198148; PubMed=8626273;
RA Furuya N., Komano T.;
RT "Nucleotide sequence and characterization of the trbABC region of the
RT Incil plasmid R64: existence of the pnd gene for plasmid maintenance
RT within the transfer region."
RT T. Bacteriol. 178:1491-1497(1996).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=91177811; PubMed=1848841;
RA Furuya N., Nisiooka T., Komano T.;
RT "Nucleotide sequence and functions of the orf operon in Incil plasmid
RT R64."
RT T. Bacteriol. 173:2231-2237(1991).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RA Komano T., Narahara K., Yoshida T., Furuya N.;
RT "The transfer region of Incil plasmid R64: similarities between R64
RT tra genes and Legionella lsm/dot genes."
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=92011438; PubMed=1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at orf of Incil plasmid R64: global
RT similarity of orf structures of Incil and IncP plasmids."
RT J. Bacteriol. 173:6612-6617(1991).
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=98053841; PubMed=9393692;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 orf region: requirement for precise
RT location of the Nika-binding sequence."
RT J. Bacteriol. 179:7291-7297(1997).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=98268996; PubMed=9603870;
RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,
RA Ogawa T., Komano T.;
RT "Purification and characterization of thin pili of Incil plasmids

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OY 113 GR0KHRLTGPCSDSYEKKP---KEFLERFKSLQKMIHOH 151
 Db 64 FNDIDREISKNCCKRQKPEIDIESFLRFDKNDKMISSH 105

RESULT 9
 ID 09VJL7 PRELIMINARY: PRT: 385 AA.
 AC 09VJL7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BG:DS02740.8 PROTEIN.
 GN BG:DS02740.8 OR CG17328.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adganyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Daventport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flocak A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Giodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Ralner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Styksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003650; AAF3516.1; -.
 DR HSSP: P08046; IALI.
 DR FlyBase: FBgn0028895; BG:DS02740.8.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; zf-C2H2; 6.
 DR SMART: SM00355; Znf_C2H2; 6.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 6.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SO SEQUENCE 385 AA; 43943 MW; 24D0EA4C5FD5DA6 CRC64;

Query Match 9.5%; Score 81; DB 5; Length 385;
 Best Local Similarity 22.2%; Pred. No. 3.5;
 Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 9;
 OY 12 VTCIAVIF-IGTIVH-KSSSGODRHHIRRMROLIDYDQKNTVNDLVEFLPAPDVT 69
 Db 24 VICNCCITRLGVAFHFKEKCEKNSD---LRLKQYIGITLESNR-----ODAT 66
 OY 70 NCEWSAFSCFOKAOLKSANTGNERNINVSIRKLKRKRPSTNAGR0KHRLTGPCSDSYE 129
 Db 67 NTD-----FVEKPLLPGRDSEEPYDAVSK-----RSR-----YQ 99
 OY 130 KRPKEFLERFKSLQKMIH-----OHLSSRTGSE 160
 Db 100 RKPPEHKKRQKRPVPMHPCYCHKSKFCIAQLTQHI--RRTGSE 144

RESULT 10
 ID 09NK60 PRELIMINARY: PRT: 414 AA.
 AC 09NK60;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BG:DS02740.8 PROTEIN.
 GN BG:DS02740.8 OR CG17328.
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RX MEDLINE=99403001; PubMed=10471707;
 RA Ashburner M., Mitra S., Roote J., Lewis S.E., Blazer R., Davis T.,
 RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
 RA Palazolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
 RA Celniker S., Rubin G.M.;
 RT "An exploration of the sequence of a 2.9-kb region of the genome of
 RT Drosophila melanogaster: the Adh region."
 RL Genetics 153:179-219(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RA Celniker S.E., Adganyani A., Arcaina T.T., Baxter E., Blazer R.G.,
 RA Butenof C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
 RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
 RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
 RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A.R., Moshrefi A.,
 RA Nixon K., Pacle J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
 RA Sethi H., Sht E., Styksas R.R., Wan K.H., Weinburg T., Zhang R.,
 RA Zieran L.L., Rubin G.M.;
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003415; AAF44996.1; -.
 DR HSSP: P08046; IALI.
 DR FlyBase: FBgn0028895; BG:DS02740.8.
 DR InterPro: IPR000345; CYTC_heme_bind.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; zf-C2H2; 6.
 DR SMART: SM00355; Znf_C2H2; 6.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN.1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 6.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SO SEQUENCE 414 AA; 47307 MW; 182657C92E2E2D1F CRC64;

Query Match 9.5%; Score 81; DB 5; Length 414;
 Best Local Similarity 22.2%; Pred. No. 3.8;
 Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 9;

OY 12 VICLWVIF-LGTLVH-KSSSGODRHMIMRMLDIDVLDKKNVNDLVEFLPAPDEVET 69
 DB 53 VICNNCTYRLGVAHFHRCQECNSD-LRLKRYLILESMT-----ODMAT 95
 OY 70 NCEWSAFSCFOKAOLKSANTGNERNINYSIKLKRKPPSTNAGRRQKRLTSCDSYE 129
 DB 96 NTD-----FVEKPLLPQRDSDDEEPVDAKYS-----RRSR-----YQ 128
 OY 130 KKPKREFLERFKSLQKMH-----OHLSTRHSE 160
 DB 129 RKPPEHKKRGKRPVKMPHTCECHKSPKCIATLOHI--RTHTGE 173

RESULT 11
 O9W756 PRELIMINARY; PRT; 187 AA.
 AC O9W756;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 INTERLEUKIN-15 PRECURSOR (INTERLEUKIN 15 PRECURSOR).
 Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCWL; TISSUE=LIVER;
 RA Burnside J., Sofer L.;
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SC; TISSUE=LIVER;
 RA Choi K.D., Lillehoj H.S., Burnside J.;
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF152927; AAD38392.1; -
 DR EMBL: AF139097; AAF61446.1; -
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15; 1
 SO SEQUENCE 187 AA; 21964 MW; 470601EBF8837095 CRC64;

Query Match 9.4%; Score 79.5; DB 13; Length 187;
 Best Local Similarity 22.2%; Pred. No. 2.1;
 Matches 34; Conservative 19; Mismatches 55; Indels 45; Gaps 6;

DB 15 LWFIFLCTLVHKKSSSG-----QDRHMIRKRLDIDVLDKKNVNDLVEFLPAPDEV 67
 OY 68 ETNCEWSAFSCF---OKAOLKSANTGNERNINYSIKLKRKPPSTNAGRRQKRLT--- 121
 DB 101 E--CQEPVNRKCFLEMKVILHECD-----IKKSRKHQVNRNIMKGNMNAFATYQ 147
 OY 122 -----CPSCDSEYKPKPKPEFLERFKSLQK 146
 DB 148 LNSTAKKCKEKEVEEKNFTETIOSFVAVIOR 180

RESULT 12
 O91Y09 PRELIMINARY; PRT; 1006 AA.
 AC O91Y09;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTOCADHERIN ALPHA C2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=99308636; PubMed=10380929;
 RA Wu Q., Maniatis T.;
 RT "A striking organization of a large family of human neural cadherin-
 RL like cell adhesion genes.";
 Cell 97:79-790(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=20202599; PubMed=10716726;
 RA Wu Q., Maniatis T.;
 RT "Large exons encoding multiple ectodomains are a characteristic
 RL feature of protocadherin genes.";
 Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=21154914; PubMed=11230163;
 RA Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz J.,
 RA Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T.;
 RT "Comparative dna sequence analysis of mouse and human protocadherin
 RL gene clusters.";
 RL Genome Res. 11:389-404(2001).
 DR EMBL: AY013769; AAK26058.1; -
 SO SEQUENCE 1006 AA; 109491 MW; EB7E29DCAF70BC1E CRC64;

Query Match 9.4%; Score 79.5; DB 11; Length 1006;
 Best Local Similarity 29.7%; Pred. No. 15;
 Matches 27; Conservative 14; Mismatches 23; Indels 27; Gaps 5;

OY 21 GTLVHSSS-----OGDRHMIRK---ROLIDVLDKKNVNDLVE-----FLPAP 64
 DB 320 GTLDYESSYQIYVATRGPPVPAHCKVLDLID-----VNDNADEVYLTDLISVP 374
 OY 65 EDVETNCEWSAFSCFOKAOLKSANTGNERNI 95
 DB 375 EDVALNTVVALLS-----VNDQSGSNRKV 399

RESULT 13
 O9J048 PRELIMINARY; PRT; 305 AA.
 AC O9J048;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE ZINC FINGER PROTEIN FLIZL.
 GN FLIZL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=LIVER;
 RX MEDLINE=21218925; PubMed=11318609;
 RA Dahm K., Nielsen P.J., Muller A.M.;
 RT "Transcripts of Flizl, a nuclear zinc finger protein, are expressed in
 RL discrete foci of the murine fetal liver.";
 Genomics 73:194-202(2001).
 DR EMBL: AF061961; AAF74513.1; -
 DR MGD; MGI:1930128; Flizl.
 DR InterPro: IPR000571; Zf-CCH.
 DR Pfam; PF00642; zf-CCH; 3.
 DR SMART; SM00356; ZNF_C3H1; 3.
 SO SEQUENCE 305 AA; 34922 MW; 2F45A0758D56245C CRC64;

Query Match 9.2%; Score 78; DB 11; Length 305;

Best Local Similarity 26.2%; Pred. No. 5.4;
Matches 37; Conservative 19; Mismatches 51; Indels 34; Gaps 7;

QY 26 KSSSG-ODRIMIRMDLIDIVOLKANYVDLPFLPAPEDVENCMASFCQKQOL 84
DB 88 ETCGSGSDNFKELQOYI---OAEEMANMAOPSLPEEPVKAGAGCTOOTAOKN-- 141
QY 85 KSANTGNERRIINVSIRKLKRPST-----NAGROKHHRLTGPCDSEYKPPK 134
DB 142 KSKAGHK-----VKOKMKRWPGTGDGSRALLKNSGRQ-----TDEPEKQPR 190
QY 135 EFLERFKSLQKMHLSR 155
DB 191 -----VMSGFIHPTVER 205

RESULT 14
096LL4
096LL4 PRELIMINARY; PRT: 319 AA.

01-DEC-2001 (TREMBLrel. 19, Created)
01-DEC-2001 (TREMBLrel. 19, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ25402 FIS, CLONE TST02870.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hoshita T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Katakami B., Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A.,
RT "NDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK058131; BAB71677.1;
SQ SEQUENCE 319 AA; 36867 MW; 682FBAE7C6CC936 CRC64;

Query Match 9.1%; Score 77; DB 4; Length 319;
Best Local Similarity 30.6%; Pred. No. 7.2;
Matches 30; Conservative 11; Mismatches 35; Indels 22; Gaps 5;

DB 66 DVETNCMSAFSCFOKAOLKSANTGNERRIINVSIRKLKRPSTNAGROKHHRLTGPC 125
DB 155 DVAS-ERDAFSC-----TYPDELNRIYFRNM-RTTPKQDAAKHISYQCPYC 202
QY 126 D-----SYKKPKPEFLERFKSLQKMHLSR 155
DB 203 NRKRAELATSAFLKOKKTLLSEF--LLOERIDEHLHTK 238

RESULT 15
09VY89
09VY89 PRELIMINARY; PRT: 421 AA.
AC 09VY89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE YP3 PROTEIN.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Berens P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacliet J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard D.R., Pui Y., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Splitter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003493; AAF48314.1;
DR Flybase: FBgn0004047; YP3.
DR InterPro: IPR000901; CPbase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00151; Lipase; 1.
DR PROSITE: PS00867; CFSASE_2; UNKNOWN_1.
SQ SEQUENCE 421 AA; 46693 MW; 5BD4A875B095DE CRC64;

Query Match 9.0%; Score 76.5; DB 5; Length 421;
Best Local Similarity 24.4%; Pred. No. 11;
Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;

QY 8 MERIVICLMIIFLTGVKSSSGODR-----HMIRMDLID----- 45
DB 1 MMSLRICLLATCLLVAAHASKDASNDRLKPTKWLTALELVNPSLNDITWERTLEMPLEQ 60
QY 46 -----VDOLKNYVNDLPPELPAPEDVENCMASFCFOKAOX-----SA 87
DB 61 GAKVTEKIYHWGQIK---HDLTSPFVSPSNVY---WIKSGGVVECKLNNYVETAKA 114
QY 88 NTGNERRIINVSIRKL-KRKPSTNAGR-----OKHRL 120
DB 115 QPFGCEDEVITVINGLPKTPSPAQOKAMRRLIOAVYOKYNL 154

Search completed: June 28, 2002, 07:44:35
Job time: 230 sec

R:Klemenz, R., Hoffmann, S.; Merenskiold, A.K.
Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
A>Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to
A:Reference number: A33541; MUID:09345536
A:Accession: A33541
A:Molecule type: mRNA
A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <KLE>
A:Cross-references: GB:M4883; NID:g201103; PIDN:AAAA0160.1; PID:g201104
R:Tomlinaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
Biochim. Biophys. Acta 1090, 1-8, 1991
A>Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal map
A:Reference number: S17657; MUID:91355215
A:Accession: S17657
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <TOM>
A:Cross-references: EMBL:X60184; NID:954200; PIDN:CAA42742.1; PID:g54201
R:Tomlinaga, S.I.
FEBS Lett. 258, 301-304, 1989
A>Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si
A:Reference number: S07054; MUID:90092495
A:Accession: S07054
A:Molecule type: mRNA
A:Residues: 1-328, 'SKECPSHIA' <TO2>
A:Cross-references: EMBL:Y07519; NID:g55517; PIDN:CAAG6812.1; PID:g55518
A>Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator
C:Genetics:
A:Gene: ST2
A:Map position: 1
A:introns: 27/1; 155/3; 210/1; 233/1; 280/2
A:Superfamily: Interleukin-1 receptor type I
C:Keywords: glycoprotein
E:1-26/Domains: signal sequence #status predicted <SIG>
F:27-33/Product: ST2 protein #status predicted <ANT>
F:60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 10.8%; Score 91.5; DB 2; Length 567;
Best Local Similarity 25.6%, Pred. No. 1.3;
Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;

OY 47 DQLKNYVDLYPERLPADVEDYTNCWSEAFSCFOKAOLKSANTGNERRIIVNSIKKLKRK 106
: : | | | | :
DB 76 DRLK-----FLPARVE-----DSGIYACV----IRSPNL-NKTGYLVNTLHK--K 113
OY 107 PPSTN-----AGRQRKHRLTCPCSDSYEKKKPRKEFLERFKSLQKKIHQH----- 151
| | | | | : : : : | | : : : : : : : : : : : : : : : :
DB 114 PPSCTIPDYLMYSTVRGSDKNKFTCTPTIDLYNMTAPVQWRCKALOEPRFAHRSYLEF 173
152 LSSRTGSE 160
: : | |
DB 174 IDNVTHDE 182

RESULT 3
B38529
nikb protein - Escherichia coli plasmid R64
C:Species: Escherichia coli
C>Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 28-Jul-2000
C:Accession: B38529
R:Furuya, N.; Nisioaka, T.; Komano, T.
J. Bacteriol. 173, 2231-2237, 1991
A>Title: Nucleotide sequence and functions of the oriT operon in IncII plasmid R64.
A:Reference number: A38529; MUID:91177811
A:Accession: B38529
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-899 <FUR>
A:Cross-references: GB:D90273; NID:g217081; PIDN:BAA1318.1; PID:g217083
C:Genetics:
A:Genome: plasmid
C:Superfamily: Escherichia coli nikb protein

```

Query Match          9.8%; Score 83; DB 2; Length 899;
Best Local Similarity 22.5%; Pred. No. 13;
Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;

Oy 27 SSSGQGDHMH1R.MROLIDIVDQKKNYNDLVPEFLPAPDEVETNCMSAF---SCFQKAQ 83
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 38 SSSQAEQPHRSRFSFLVYATRLRN-----ESFVALVDVKKDCGEWNVFQGVCFNHCT 91

Oy 84 LKSANTGNMERIINISIKKLKRKPPSTNAGRQKHRL---TCP-----SCDSTEKKPK 134
      : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 92 SLETAAMEMETI-----ARQAHYAKDPPDPVFHYITLSSQSHESPE 133

Oy 135 EFLERFKSLQKM---IHQHLSSRTHGSEDS 162
Db 134 QIYDSVRTLLKSLGLADHQVSA-VHTDTDN 163

RESULT 4
ABXL72
74K albumin precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence,revision 31-Dec-1993 #text,change 22-Jun-1999
C:Accession: B41682; S02693; A05288
R:MoKallits, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.
Mol. Endocrinol. 3, 464-473, 1989
A>Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic
      e during development.
A:Reference number: A41682; MUID:89313788
A:Accession: B41682
A:Molecule type: mRNA
A:Residues: 3-607 <MOS>
A:Cross-references: GB:M1442; NID:g213930; PTD:AAA637.1; PID:g213931
R:Schorpp, M.; Doebebling, U.; Wagner, U.; Ryffel, G.U.
J. Mol. Biol. 199, 83-93, 1988
A>Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. D
      A:Reference number: S02692; MUID:88172470
A:Accession: S02693
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-48 <SCH>
A:Cross-references: EMBL:Z26826
R:Wolfe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata,
      Bur. J. Biochem. 146, 489-496, 1985
A>Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabiliza
      A:Reference number: A05288; MUID:85126974
A:Accession: A05288
A:Molecule type: mRNA
A:Residues: 459-502, '1', 504-557 <WOL>
A:Cross-references: GB:M28276
A:Note: the authors translated the codon TAT for residue 63 as Thr
      C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppe
      mones (weak bonds with these hormones promote their transfer across the membranes), t
      C:Genetics:
A:Introns: 27/1
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-607/Product: 74K serum albumin #status predicted <MAT>
F:32-201/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:30/Binding site: copper (His) #status predicted
F:80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-3
      F:256/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match          9.6%; Score 82; DB 1; Length 607;
Best Local Similarity 24.2%; Pred. No. 10;
Matches 38; Conservative 19; Mismatches 50; Indels 50; Gaps 6;

Oy 44 DIVDQKKNYNDLVPEF-----LPAPDEVETNCMSAFSCF---QKAQKLSAN 88

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Db 72 EINFPAKSCINDKPECEKPVGTLFEDKLCADPAVGVYEMSKCECAKODPERAOCFAH 131
Query Match 9.3%; Score 79; DB 2; Length 206;
Best Local Similarity 26.1%; Pred. No. 6.1;
Matches 29; Conservative 18; Mismatches 48; Indels 16; Gaps 3;
Y 48 OLKRVNDLVEFLPAPEDVETNCENSAFSCFOKAOLKSANTGNENKINIVSIKKLRKP 107
Db 12 QATSVNGLLSNLLPGVYKIRANNGKTSVNNGSKAOLIDRLKRVOLQNRDVRKIRKKC 71
Y 108 PSTNAGRQKRLTCPSDCSYEKKRPKEFLERF--KSLQKIHQHSRT 156
Db 72 KLVKKKKYKKRKL-----DKQLQLAKHOVLK--HQHEGTLT 108
RESULT 6
A25876
vitellogenin III precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: yolk polypeptide yIII; yolk protein 3
C:Date: 04-Mar-1988 #sequence_revision 12-May-1994 #text_change 20-Aug-1999
C:Accession: A25876; A27388
R:Van, Y.L.; Kunert, C.J.; Postlethwait, J.H.
Nucleic Acids Res. 15, 67-85, 1987
A:Title: Sequence homologues among the three yolk polypeptide (Yp) genes in Drosophila m
A:Reference number: A25876; MUID:87146365
A:Accession: A25876
A:Molecule type: DNA
A:Residues: 1-420 <YAN>
A:Cross-references: GB:X04754; NID:98844; PIDN:CAA28451.1; PID:98845
R:Garabedian, M.J.; Shirra, A.D.; Bowes, M.; Wensink, P.C.
Gene 55, 18, 1987
A:Title: The nucleotide sequence of the gene coding for Drosophila melanogaster yolk pro
A:Reference number: A27388; MUID:87305580
A:Accession: A27388
A:Molecule type: DNA
A:Residues: 1-420 <GAR>
A:Cross-references: GB:M15898; NID:9158815; PIDN:AAA29024.1; PID:9158816
C:Genetics:
A:Gene: FlyBase:Yp3
A:Cross-references: FlyBase:Fbgn0004047
C:Superfamily: Insect vitellogenin
C:Keywords: egg yolk; glycoprotein; phosphoprotein; sulfoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>

Query Match 9.0%; Score 76.5; DB 2; Length 420;
Best Local Similarity 24.4%; Pred. No. 22;
Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;
Y 8 MERVICLAWIFLGTIVHKSSSGQDR-----HMIRKROLIDI----- 45
Db 1 MMSLRICLALTCLVAHAASKOASNDRLKPTKWLTALENNPNSLNDIWERLENPLEQ 60
Y 46 -----VDOLKRVNDLVEFLPAPEDVETNCENSAFSCFOKAOLK-----SA 87
Db 61 GARVIEKIVHVGQIK--HDLTPSFVSPSNVPV--WIKSNGQVCEKLNMYETAKA 114
Y 88 NTGNENRIINVSIKKL-KRKPSTNAGR--OKHRL 120
Db 115 QPGFGEDEVITVLTGLPKTSPAQKAMRRLQAYVQKYNL 154
RESULT 7
S60441
hypothetical protein YGR150C - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G6642
C:Species: Saccharomyces cerevisiae
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 29-Oct-1999
C:Accession: S60441; S64459
R:Skala, J.; Nawrocki, A.; Goffeau, A.
Yeast 11, 1421-1427, 1995
A:Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacc
A:Reference number: S60435; MUID:96158062
A:Accession: S60441
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-864 <SKA>
A:Cross-references: EMBL:X85807; NID:91045249; PIDN:CAA59808.1; PID:91045256
R:Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talla, E.; Nawrocki, A.;
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64428
A:Accession: S64459
A:Molecule type: DNA
A:Residues: 1-864 <YAN>
A:Cross-references: EMBL:Z72935; NID:91323253; PIDN:CAA97164.1; PID:e243709; PID:9132
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 7R
Query Match 9.0%; Score 76.5; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 48;
Matches 43; Conservative 22; Mismatches 59; Indels 67; Gaps 8;
Y 2 RSSPGNNRIVIC-----LWVIFGTIVHKSSSGQDRHMRROLIDIVOLKRVNDLY 57
Db 5 RCGPKNN--VLCEFPOLFESKRLINK-----RKYTLQTEDE-KNMKGSLIS 49
Y 58 PEFLPAPEDVETNCENSAFSCFOKAOLKSANTGNENRIINVSIIKKLRKPSTNAGRQK 117
Db 50 KNNIITPEVE-----FKLAQLREFSNTLKRIRINTK-----SYNSDGHQS 90
Y 118 HRLTSCDSYEKKRPK-----EFLERKSLQKMIHQ----- 150
Db 91 NSIAPISDSRNVNVTSSVPNEEKSMLSDLIHSSFLEKMDHLVPKVIRERVADDITL 150
Y 151 --HLSSRTGS 159
Db 151 AKNLFDRSHSN 161
RESULT 8
S42022
ureidoglycolate hydrolase (Ec 3.5.3.19) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YIR032c

C:Species: *Saccharomyces cerevisiae*
C:Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 21-Jul-2000
C:Accession: S42022; S48494
R:YOO, H.S.; Cooper, T.G.
Yeast 7, 693-698, 1991
A:Title: The ureidoglycolate hydrolase (DAL3) gene in *Saccharomyces cerevisiae*.
A:Reference number: S42022; MUID:92133160
A:Accession: S42022
A:Molecule type: DNA
A:Residues: 1-195 <YOO>
A:Cross-references: EMBL:M64778; NID:g171369; PIDN:AAA3025.1; PID:g171370
R:Rowley, K.
Submitted to the EMBL Data Library, October 1994
A:Reference number: S48478
A:Accession: S48494
A:Molecule type: DNA
A:Residues: 1-195 <ROW>
A:Cross-references: GB:z47047; EMBL:Z38061; NID:g603997; PID:g763377; MIPS:YIR032C
C:Genetics:
A:Gene: SGD:DAL3
A:Cross-references: SGD:S0001471; MIPS:YIR032C
Map position: 9R
Keywords: allantoin degradation; hydrolase; lipoprotein; methylated carboxyl end; pre-
P199/Binding site: farnesyl (Cys) (covalent) #status predicted
P199/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match	8.9%	Score 76	DB 2	Length 195
Best Local Similarity	27.6%	Pred. No. 11		
Matches 24	Conservative 14	Mismatches 29	Indels 20	Gaps 3

```
OY      24 VHKSSOGQDRHMRMRLIDIVDQLKNVYNVDLPPELPAPEDETNCESWASFCFOKAQ 83
        : | ::|| |::| |::| |
Db     33 LEKGANQGT--AIKLLQ-----VSQVENKSTSKVP-----MNWLFRCPQPH 72
```

```
QY      84 LKSANTGNNERIINVSIIKKLRKPPST 110
          | : : | : | | : : | |
Db      73 LNRVFTQGSNOAISHSIKYLEKHPGST 99
```

RESULT 9
S42632
Flt-1s protein precursor - rat

C: Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C: Accession: S42632
R: Bergers, G.; Reiterstorfer, A.; Braselmann, S.; Graninger, P.; Busslinger

Title: Alternative promoter usage of the Fos-responsive gene *Fil-1* generates mRNA isoforms
 Accession: S42632; MUID: 94178260
 Reference number: S42632

A:Residues: 1-336 <BER>
A:Cross-references: GIB:U04319; NID:q488278; PIDN:AAA67172.1; PID:q488279
C:Superfamily: vaccinia virus B15R protein; immunoglobulin homology

Query Match	8.9%	Score	75.5	DB	2	Length	336
Best Local Similarity	22.2%	Pred.	No.	22			
Matches	30	Conservative	26	Mismatches	42	Indels	37
						Gaps	6

```

Qy 43 IDIDQKNTVNDLP-----EFLPADEVETNCENSAFSCQKQKLSAN 88
      | : : : : : : : : : : : : : : : : : : : : : :
Db 49 INPEWYYSNTNERIPQKRNRIFVSRDLKFLPAKVE-----DSGIYTCVIRSP-ESIK 102

```

```
QY      89 TGNNERIINVSIIKKLRKPP-----STNAGRQRQHRLTSCSDSYEKKPKPELE 138
       || :||| | :|| | | : :||| : | ::
Db     103 TGS-----LNTIlyk--RPNCKIPDYMYSTVDGSDKNSKITCPITALYNWTAPOWMFK 155
```

QY	139	REFSLQKMIHQHLS	153
		:	:
Db	156	NCKALQGPFRRAHMS	170

RESULT 10
T28957
hypothetical protein F45F2.11 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28957
R:Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid F45F2.
A:Reference number: Z20548
A:Accession: T28957
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-406 <DNA>
A:Cross-references: EMBL:U64845; PIDN:AAC48032.1; GSEDB:GN00023; CESP:F45F2.11
A:Experimental source: strain Bristol N2; clone F45F2
C:Genetics:
A:Gene: CESP:F45F2.11
A:Map position: 5
A:introns: 1/2; 24/2; 143/3; 307/2; 338/2

Query Match	8.98;	Score 75.5;	DB 2;	Length 406;
Best Local Similarity	20.5%;	Pred. No. 26;		
Matches	38;	Conservative	23;	Mismatches 55; Indels 69; Gaps 7,

```

Qy 26 KSSSGGQDRHMTIRMRLDIDVQLKNYVNDLVPFELP----- 62
    ||| | : : | | |||
Db 13 KSSPQSDENFQKRLQWCKIRLELK-----TPEFLNSESSELETKNKSQIQKCGENEG 66

```

```

QY 63 -----APEDVETNCSEW-----SAPSCFQKAKQTSANTGNNER 94
      | : : : | | | :
Db 67 ENEEKCEFRPVYTPNEIDSHKEMWRLMLKLEYKRGSGRGAFFPPPPPLPSMTAAASNA 122

```

```

QY      95 IINSAIKILKR-----KPSPTNAGRÖKHRLTQPCSDSEYKEKPEFLEREKSLÖKM 147
      :      : : : : | : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 VSFNPFDEVRAAQAKTAKSPSTSLERAQR-CPA-DQÖPLPRPHIYENIIRTLP-- 182

```

QY	148	THQHL	152
		::	
Db	183	-HQYI	186

```

RESULT      11
S24407
formin isoform IV - mouse

```

Cidate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1995
C:Accession: S24407
R:Jackson-Grusby, L.; Kuo, A.; Leder, P.
Genes Dev. 6, 29-37, 1992

A: Molecule type: mRNA
 A: Accession: S24407
 A: Reference number: S24407; MUID: 92112033
 A: Title: A variant limb deformity transcript expressed in the embryonic mouse limb development

Query Match 8.9%; Score 75.5; DB 2; Length 1206;
A/Cross-References: EMBL:AO2375; NID:gcjccz; FIDN:CAAA4244.1; FID:gcjccz

Matches 37; Conservative 41; mismatches 69; Indels 21; Gaps 8

2 RSPG--NMERT--VICIMVIFLCTLVHKSSQCG-DRHMIRMQLIDIVDQKNYVN-- 54

Db 953 RASGLLHHKSVKDILALILAFGNYNANGNRIRGQAGCYSLEILPKLDVKSRRNGMNLV 1012

QY 55 DLVEELLPAEDVETNCESAFSCFOKAQLSANTGNNRIINWSIKKLKRRPSTNAGR 114

Db 1013 DYVVKYYLRYDQAGTDKSVFPLPEPQDFFLASQVKFEEDLLK-DLRKLRQLEAS---- 1067

Fri Jun 28 07:58:55 2002

us-09-825-561a-10.rpr

Page 6

[illegible]

Search completed: June 28, 2002, 07:42:56
Job time: 131 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:43:20 ; Search time 20.33 Seconds
(without alignments)
308.537 Million cell updates/sec

Title: us-09-825-561a-10

Perfect score: 850
Sequence: 1 MRSSPGMEXIVICLAWIFL.....LLOKMTIHOHLSTRHSGSDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 105224 seqs, 36719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106.5	12.5	162	1 IL15_FELCA	097687 felis silve
2	99.5	11.7	162	1 IL15_HUMAN	P40933 homo sapien
3	94.5	11.1	162	1 IL15_CERAE	P40221 cercoptilhec
4	94.5	11.1	162	1 IL15_MACMU	P48092 macaca mula
5	91.5	10.8	337	1 IRL1_MOUSE	P14719 mus musculu
6	90.5	10.6	162	1 IL15_BOVIN	Q28028 bos taurus
7	90.5	10.6	162	1 IL15_SHEEP	O9X316 ovvis aries
8	82	9.6	607	1 ALB2_XENLA	P14872 xenopus lae
9	80.5	9.5	162	1 IL15_PIG	O95253 sus scrofa
10	79	9.3	206	1 YIM7_YEAST	P40470 saccharomyc
11	78	9.2	741	1 IDH_AZOVI	P16100 azotobacter
12	77	9.1	856	1 KMS5_HUMAN	Q02241 homo sapien
13	76.5	9.0	420	1 VIR3_DROME	P06607 drosophila
14	76.5	9.0	864	1 YG3M_YEAST	P48237 saccharomyc
15	76	8.9	195	1 ALIA_YEAST	P32459 saccharomyc
16	75.5	8.9	133	1 IL4_FELCA	P55030 felis silve
17	75.5	8.9	1206	1 FM14_MOUSE	Q05859 mus musculu
18	75	8.8	334	1 LCMT_HUMAN	Q9U1C8 homo sapien
19	74.5	8.8	441	1 FUS6_ARATH	P45432 arabidopsi
20	74.5	8.8	789	1 YK25_CAEEL	P34332 caenorhabdi
21	73.5	8.6	162	1 IL15_MOUSE	P48346 mus musculu
22	73.5	8.6	472	1 IFM2_HUMAN	P09913 homo sapien
23	73.5	8.6	477	1 CCR3_RABIT	P54286 oryctolagus
24	73.5	8.6	484	1 CCR3_HUMAN	P54284 homo sapien
25	73.5	8.6	484	1 CCR3_RAT	P54287 rattus norv
26	73	8.6	304	1 IF2A_YEAST	P20459 saccharomyc
27	72.5	8.5	162	1 IL15_RAT	P97604 rattus norv
28	72	8.5	262	1 Y069_NPVAC	P41469 autographa
29	71.5	8.4	484	1 CCR3_MOUSE	P54285 mus musculu
30	71.5	8.4	2758	1 IP3R_HUMAN	O14643 homo sapien
31	71	8.4	805	1 AHR_MOUSE	P30561 mus musculu
32	70	8.2	403	1 IFI3_MOUSE	Q64345 mus musculu
33	70	8.2	739	1 BAC1_MOUSE	P97302 mus musculu

34	70	8.2	1222	1 YNP3_CAEEL	Q10947 caenorhabdi
35	70	8.2	1230	1 SMC3_YEAST	P47037 saccharomyc
36	70	8.2	1636	1 BUD3_YEAST	P25558 saccharomyc
37	69.5	8.2	219	1 Y413_RICPR	Q942b9 rickettsia
38	69.5	8.2	678	1 Y564_TREPA	O83575 treponema p
39	69.5	8.2	1468	1 FBN1_MOUSE	O05860 mus musculu
40	69.5	8.2	1750	1 Y832_METUA	O58242 methanococc
41	69	8.1	132	1 IL4_CANFA	O77762 canis fami
42	69	8.1	568	1 FTS1_BUCAP	O85297 buchnera ap
43	69	8.1	932	1 PMS1_HUMAN	P54277 homo sapien
44	68.5	8.1	464	1 N2B_HAEIR	P46441 haematobia
45	68.5	8.1	655	1 YDH2_SCHPO	Q92347 schizosacch

ALIGNMENTS

RESULT 1	ID	IL15_FELCA	STANDARD:	PRT:	162 AA.
AC	097687	IL15_FELCA			
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DE	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Interleukin-15 precursor (IL-15).				
GN	IL15.				
OS	Felis silvestris catus (Cat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
OX	NCBI_Taxid=9685;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lymph node;				
RA	Barger A.B., Dean G.A., Layoy A.S.;				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-				
CC	IMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15				
CC	WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R				
CC	GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF108148; AAD05268.1; -				
DR	InterPro; IPR003443; Interleukin_15.				
DR	Pfam; PF02372; IL15; 1.				
FW	Cyclokin; Glycoprotein; Signal.				
FT	SIGNAL 1 29				
FT	PROPEP 30 48				
FT	POTENTIAL.				
FT	CHARN 49 162				
FT	DISULFID 83 133				
FT	DISULFID 90 136				
FT	CARBOHYD 104 104				
FT	CARBOHYD 127 127				
FT	SEQUENCE 162 AA; 18412 MW; D8C7CE7FA0110DD CRC64;				
QY	14 CLAWFLGTU---VHKSSGOGDHRMRLDIDYDLKYNVNDLVPEFLPAEVEVETN 70				
DB	30 CIPVFILSCINAGLPKTEANMD--VTSDLKIIDKIISIHIDATLYTE-----SVYHN 82				
QY	71 CEWSAFSCF---OKAOLKSANTGNERNRILNVSIRKILRRKPPSTNAGRRQKRLT---CP 123				

Query Match 12.5%; Score 106.5; DB 1; Length 162;
Best local similarity 26.0%; Pred. No. 0.0042;
Matches 38; Conservative 25; Mismatches 58; Indels 25; Gaps 6;

```

DB      83 CQVYAMKCFLELHAVISSEKNETIHQTVENII-----LANSGLSSNRNITETGCK 134
QY      124 SCDSYEKKPKPEFLERFSLOKMH 149
DB      135 ECEELFEKNIKRFLQSFVHIQMFN 160

RESULT 2
ID      IL15_HUMAN
ID      IL15_HUMAN STANDARD: PRT: 162 AA.
AC      P40933; G93058; 043512; 000440; Q9UBA3;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Interleukin-15 precursor (IL-15).
GN      IL15.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (IL15-S48AA ISOFORM).
RC      TISSUE-Bone marrow;
RX      MEDLINE=94233380; PubMed=8178155;
RA      Grabstein K.K., Eisenman J., Sheenbeck K., Rauch C.,
RA      Srihvasan S., Fung V., Beers C., Richardson J., Schoenborn M.A.,
RA      Abdiel M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
RA      Gail J.G.;
RT      "Cloning of a T cell growth factor that interacts with the beta chain
RT      of the interleukin-2 receptor.";
RL      Science 264:965-968(1994).
[2]
SEQUENCE FROM N.A. (IL15-S48AA ISOFORM).
RA      Krause H., Jandrig B., Wernicke C., Bulfone-Paus S., Pohl T.,
RA      Diamantstein T.;
RL      Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).
RC      TISSUE-Lung cancer;
RX      MEDLINE=96218668; PubMed=8668345;
RA      Meazza R., Verdiani S., Bissonti R., Coppolecchia M., Gaggero A.,
RA      Orenzo A.M., Colombo M.P., Azzarone B., Ferrini S.;
RT      "Identification of a novel interleukin-15 (IL-15) transcript isoform
RT      generated by alternative splicing in human small cell lung cancer
RT      cell lines.";
RL      Oncogene 12:2187-2192(1996).
[4]
SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).
RC      TISSUE-Testis;
RX      MEDLINE=98070771; PubMed=9405632;
RA      Tagaya Y., Kurys G., Thies T.A., Lost J.M., Azimi N., Hanover J.A.,
RA      Bamford R.N., Waldmann T.A.;
RT      "Generation of secretable and nonsecretable interleukin 15 isoforms
RT      through alternate usage of signal peptides.";
RL      Proc. Natl. Acad. Sci. U.S.A. 94:1444-1449(1997).
[5]
SEQUENCE FROM N.A. (ISOFORM 3).
RA      Meazza R., Ferrini S.;
RT      "Expression of two IL-15 mRNA isoforms in human tumors does not
RT      correlate with secretion: role of different signal peptides.";
RL      Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE OF 49-162 FROM N.A.
RC      TISSUE-Epidermis;
RA      Sorel M.A., Jacques Y.;
RT      "IL15 expression in human keratinocytes.";
RL      Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC      LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC      WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC      GAMMA BUT NOT IL-2R ALPHA.
CC      -1- SUBCELLULAR LOCATION: SECRETED (IL15-S48AA). IL15-S21AA IS NOT

```

```

CC      SECRETED, BUT RATHER IS STORED INTRACELLULARLY, APPEARING IN THE
CC      NUCLEUS AND CYTOPLASMIC COMPONENTS.
CC      -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; IL15-S48AA (SHOWN HERE),
CC      IL15-S21AA AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: MOST ABUNDANT IN PLACENTA AND SKELETAL MUSCLE.
CC      IT IS ALSO DETECTED IN THE HEART, LUNG, LIVER AND KIDNEY. IL15-
CC      S21AA IS PREFERENTIALLY EXPRESSED IN TISSUES SUCH AS TESTIS AND
CC      THYMOS.
CC      -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC      -1- DATABASE: NAME-R&D systems' cytokine source book: IL15;
CC      WWW="http://www.indsystems.com/asp/g-sitebuilder.asp?bid=209".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
DR      EMBL: U14407; AAA21551.1; -
DR      EMBL: X91233; CAA62616.1; -
DR      EMBL: X94223; CAA63914.1; -
DR      EMBL: X94222; CAA63913.1; -
DR      EMBL: AF031167; AAB97518.1; -
DR      EMBL: Y09908; CAA71044.1; -
DR      EMBL: Z38000; CAA66100.1; -
DR      MIM: 600554; -
DR      Interpro: IPR003443; Interleukin_15.
DR      Pfam: PF02372; IL15; 1.
KW      Cytokine. Glycoprotein. Signal. Alternative splicing.
FT      SIGNAL 1 29
FT      PROPEP 30 48
FT      CHAIN 49 162
FT      DISULFID 83 133
FT      DISULFID 90 136
FT      CARBOHYD 127 127
FT      VARSPPLIC 1 37
FT      FT
FT      VARSPPLIC 1 47
FT      FT
FT      CONFLICT 141 141
FT      SEQUENCE 162 AA; 18086 MW; 0CEB0520C1D8379E2 CRC64;

Query Match 11.7%; Score 99.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0 019;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY      43 IDIVDQIKNTVNDLPVPE-----LPAPEDVETNCWESAFCF---OKAQLSANTGNE 93
DB      51 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCRYAMKCFLELQVISTLEGDSIDH 109
QY      94 RITVNSIKKLKRKPRPTNAGRROKHRLTCPSQDSYEKKPKPEFLERFSLOKMH 149
DB      110 TVENLII--LANSLSNGNVTES---GCKECELFEKNIKRFLQSFVHIQMFN 160

RESULT 3
ID      IL15_CERAE
ID      IL15_CERAE STANDARD: PRT: 162 AA.
AC      P40221;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Interleukin-15 precursor (IL-15).
GN      IL15.
OS      Cercopithecus aethiops (Green monkey) (Givet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;

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RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 49-81.
RC TISSUE=Kidney;
RX MEDLINE=94233380; PubMed=8178155;
RA Strabstein K.H., Eisenman J., Shanebeck K., Rauch C.,
RA Strabstein S., Fung V., Beers C., Richardson J., Schoenborn M.A.,
RA Adiel M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
RA Gird J.G.;
RT "Cloning of a T cell growth factor that interacts with the beta chain
RT of the Interleukin-2 receptor.";
RL Science 264:965-968(1994).
CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U03099; AAA18416.1; -
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 48
FT CHAIN 49 162 INTERLEUKIN-15.
FT DISULFID 83 133 POTENTIAL.
FT DISULFID 90 136
FT CARBOHYD 127 127 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT SEQUENCE 162 AA; 18222 MW; 1BF9A82644E1C9B7 CRC64;
SQ
Query Match 11.1%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.054;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;
QY 43 IDIVDLKNTVNDLVEF-----LPAPDEVETNCMSAFSCF-----QKALKSANTGNE 93
DB 51 VNVISDLKK-IEDLQSMHIDATLTYESDVHPSCKYTKAKCFLELQVISHESGDTIHD 109
94 RIINVSIKKLKRPSTNAGRQKHRLTCPDSCSYEKKPKPEFLERKSLQKMIH 149
DB 110 TVENLIIT--LANNIISSNGNTES---GCKECELKEKNIKEFLQSFVHIYVMPFIN 160
RESULT 4
ID IL15_MACMU STANDARD; PRT; 162 AA.
AC P48092;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Eukarya mulatta (Rhesus macaque).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Cercopitheciinae; Primates; Catarrhini; Cercopitheciidae;
OC NCBI_TaxID=9544;
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Vulliamer F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";

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RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19843; AAB60398.1; -
DR EMBL: AB000555; BAA19149.1; -
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 48
FT CHAIN 49 162 INTERLEUKIN-15.
FT DISULFID 83 133 POTENTIAL.
FT DISULFID 90 136
FT CARBOHYD 127 127 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT VARIANT 5 5 K -> T.
FT VARIANT 31 31 I -> T.
FT SEQUENCE 162 AA; 18194 MW; D233CF7F6F0188C01 CRC64;
SQ
Query Match 11.1%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.054;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;
QY 43 IDIVDLKNTVNDLVEF-----LPAPDEVETNCMSAFSCF-----QKALKSANTGNE 93
DB 51 VNVISDLKK-IEDLQSMHIDATLTYESDVHPSCKYTKAKCFLELQVISHESGDTIHD 109
94 RIINVSIKKLKRPSTNAGRQKHRLTCPDSCSYEKKPKPEFLERKSLQKMIH 149
DB 110 TVENLIIT--LANNIISSNGNTES---GCKECELKEKNIKEFLQSFVHIYVMPFIN 160
RESULT 5
ID IRL_MOUSE STANDARD; PRT; 337 AA.
AC P14719;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin 1 receptor-like 1 precursor (ST2 protein) (T1 protein)
DE (lymphocyte antigen 84).
GN ILIRL1 OR ST2 OR STP2 OR LY84.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=90092495; PubMed=2532153;
RA Tomimaga S.;
RT "A putative protein of a growth specific cDNA from BALB/C-3T3 cells
RT is highly similar to the extracellular portion of mouse interleukin 1
RT receptor.";
RL Febs Lett. 258:301-304(1989).
RN [2]

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RC SEQUENCE FROM N.A.
RC STRAIN=C3H/HE; TISSUE=Spleen;
RX MEDLINE=91355215; PubMed=1832015;
RA Tomiunga S.I., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Tetsuka T.;
RT "Molecular cloning of the murine ST2 gene. Characterization and
RT chromosomal mapping.";
RL Biochim. Biophys. Acta 1090:1-8(1991).
RM [3]
RM SEQUENCE FROM N.A.
RX MEDLINE=8934536; PubMed=2527364;
RA Klemenz R., Hoffmann S., Wieruskold A.K.;
RT "Serum- and oncoprotein-mediated induction of a gene with sequence
RT similarity to the gene encoding carcinoembryonic antigen.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5708-5712(1989).
CC -1- FUNCTION: POSSIBLY INVOLVED IN REGULATION OF T-LIMPHOCYTE
CC ACTION.
CC -1- DEVELOPMENTAL STAGE: GROWTH-SPECIFIC EXPRESSION, G1-PHASE OF
CC CELL CYCLE.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.
CC
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CC -----
CC DR EMBL, Y07519; CAA68812.1; -
CC DR EMBL, X60184; CAA42742.1; -
CC DR EMBL, M24843; AAA40160.1; -
CC DR PIR, S07054; S07054.
CC DR MGD; MGI:98427; I11r11.
CC DR InterPro: IPR003306; IG_MHC.
CC DR InterPro: IPR003598; IG_C2.
CC DR Pfam; PF00047; Ig_3.
CC DR SMART; SM00408; IGC2; 2.
CC DR Immunoglobulin domain; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 26
CC FT CHAIN 27 337
CC FT DOMAIN 35 100
CC FT DOMAIN 132 194
CC FT DOMAIN 233 315
CC FT DISULFID 42 93
CC FT DISULFID 139 187
CC FT DISULFID 240 308
CC FT CARBOHYD 60 60
CC FT CARBOHYD 101 101
CC FT CARBOHYD 107 107
CC FT CARBOHYD 146 146
CC FT CARBOHYD 176 176
CC FT CARBOHYD 194 194
CC FT CARBOHYD 225 225
CC FT CARBOHYD 259 259
CC FT CARBOHYD 278 278
CC FT VARIANT 192 192
CC FT SEQUENCE 337 AA; 38502 MW; 7574372722486926 CRC64;
CC
CC Query Match 10.8%; Score 91.5; DB 1; Length 337;
CC Best Local Similarity 25.6%; Pred. NO. 0.23;
CC Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;
CC
CC Oy 47 DOLKAYVNDLVPEFIPAEDEVETNCEWMSAFSCFOAKOLKSANTGNNERLIINYSIKKLKRX 106
CC |::| |::| :::| |::| |::| |::| |
CC Db 76 DRLK-----ELPAVE-----DSGLYACV-----IRSPVL-NKTGYLVNTYIHK---K 113
CC |::| |::| :::| |::| |::| |::| |
CC Oy 107 PPSTN-----AGRRQKHRLTCPSCDSEYKRRPKPEFLERFSLLQKMHQ----- 151
CC |::| |::| :::| |::| |::| |::| |
CC Db 114 PPSCHIPDYLMYSTVRGSDKNFKIKTCPTIDLYNMTAPVQWFKNCALQDPRFAHRYLF 173

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QY	152	LSRTHGSE	160
DB	174	IDNVTTHDDE	182
RESULT 6			
IL15_BOVIN	6	STANDARD:	PRT: 162 AA.
ID	IL15_BOVIN	STANDARD:	PRT: 162 AA.
AC	028028:		
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	15-DEC-1998	(Rel. 37, Last annotation update)	
DE	Interleukin-15 precursor (IL-15).		
GN	IL15.		
OS	Bos taurus (bovine).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=HOLSTEIN:		
RC	MEDLINE=97426124; PubMed=9282828;		
RA	Canalis A., Gabbarre L.C., Boyd P.C., Almeria S., Zarlenga D.S.;		
RT	"Cloning and expression of bovine Interleukin-15: analysis and		
RT	modulation of transcription by exogenous stimulation."		
RL	J. Interferon Cytokine Res. 17:473-480(1997).		
CC	-1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-		
CC	LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15		
CC	WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R		
CC	GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.		
CC	-----		
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: U42433; AAA85130.1; .		
DR	InterPro: IPR003443; Interleukin_15.		
DR	Pfam: PF02372; IL15; 1.		
DR	Cytokine; Glycoprotein; Signal.		
KW	SIGNAL	1	29
FT	PROPEP	30	48
FT	CHAIN	49	162
FT	DISULFID	83	133
FT	DISULFID	90	136
FT	CARBOHYD	104	104
FT	CARBOHYD	113	113
FT	CARBOHYD	121	121
FT	CARBOHYD	127	127
SEQUENCE	162 AA; 18554 MM; 6633CAA329EB8302 CRC64;		
Query Match 10.6%; Score 90.5; DB 1; Length 162;			
Best Local Similarity 25.5%; Pred. No. 0.13;			
Matches 28; Conservative 17; Mismatches 58; Indels 7; Gaps 3;			
QY	45	IYDOLKNVNDVPE-----LPADEDVETNCEMSAFSCFOKAQLKSANTGNERRIIVNS	99
DB	53	VINDLKT-IEHLIGSIHMDATLYTSDAHPNCKVYNAQCFLLELYVILHESKNATYYEL-	110
QY	100	IKKLKKPDPSTNAGRRQRHRLTQPSCDSEYKKPKPEFLERFKSLQKKIH	149
DB	111	IEHLTFLANSNLSIENKTELQCKCECELEERSIKEFLKSPVHIQMFILN	160
RESULT 7			
IL15_SHEEP			

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ID IL15_SHEEP STANDARD; PRT; 162 AA.
AC O9XSJ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Casey G.J., Chaplin P.J.;
RT "Isolation of interleukin-15 mRNA transcripts from T and B cells
RL circulating in effluent lymph."
J. Interferon Cytokine Res. 0:0-0(1999).
-1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC -----
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CC -----
DR EMBL: AF149700; AAD37425.1;
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15.1.
DR Cytokine; Glycoprotein; Signal.
KM SIGNAL 1 29
FT PROPEP 30 48 POTENTIAL.
FT CHAIN 49 162 POTENTIAL.
FT DISULFID 83 133 INTERLEUKIN-15.
FT DISULFID 90 136 POTENTIAL.
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 162 AA; 18510 MW; 87195650E45F1E5D CRC64;

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Query Match 10.6%; Score 90.5; DB 1; Length 162;
Best Local Similarity 22.0%; Pred. No. 0.13;
Matches 33; Conservative 24; Mismatches 74; Indels 19; Gaps 4;

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OS Xenopus laevis (African Clawed Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE OF 3-607 FROM N.A.
RX MEDLINE=89313788; PubMed=2747653;
RA Moskaitis J.E., Sargent T.D., Smith L.H. Jr., Pastori R.L.,
RA Schoenberg D.R.;
RT "Xenopus laevis serum albumin: sequence of the complementary
RT deoxyribonucleic acids encoding the 68- and 74-kilodalton peptides
RT and the regulation of albumin gene expression by thyroid hormone
RT during development."
RL Mol. Endocrinol. 3:464-473(1989).
RN [2]
RP SEQUENCE OF 1-48 FROM N.A.
RX MEDLINE=88172470; PubMed=2451026;
RA Schorpp M., Doeberling U., Wagner U., Ryffel G.U.;
RT "5'-flanking and 5'-proximal exon regions of the two Xenopus albumin
RT genes. Deletion analysis of constitutive promoter function."
RL J. Mol. Biol. 199:83-93(1988).
RN [3]
RP SEQUENCE OF 459-557 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=85126974; PubMed=3971963;
RA Wolffe A.P., Glover J.F., Martin S.C., Tenniswood M.P.R.,
RA Williams J.L., Tata J.R.;
RT "Deactivation of transcription of Xenopus 74-kDa albumin genes and
RT destabilization of mRNA by estrogen in vivo and in hepatocyte
RL cultures."
RL Eur. J. Biochem. 146:489-496(1985).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -----
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CC -----
DR EMBL: M21442; AAA49637.1;
DR EMBL: M28276; AAA49642.1;
DR PIR: B41682; ABXL72.
DR HSSP: P02768; IBJ5.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot. 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin. 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 24 POTENTIAL.
FT CHAIN 25 607 74 KDA SERUM ALBUMIN.
FT REPEAT 29 211 1.
FT REPEAT 217 403 2.
FT REPEAT 409 601 3.
FT METAL 30 30 COPPER (BY SIMILARITY).
FT DISULFID 80 88 BY SIMILARITY.
FT DISULFID 101 117 BY SIMILARITY.
FT DISULFID 116 127 BY SIMILARITY.
FT DISULFID 147 192 BY SIMILARITY.
FT DISULFID 191 200 BY SIMILARITY.

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FT DISULFID 223 269 BY SIMILARITY.
 FT DISULFID 268 276 BY SIMILARITY.
 FT DISULFID 288 302 BY SIMILARITY.
 FT DISULFID 301 312 BY SIMILARITY.
 FT DISULFID 339 384 BY SIMILARITY.
 FT DISULFID 382 392 BY SIMILARITY.
 FT DISULFID 415 461 BY SIMILARITY.
 FT DISULFID 460 471 BY SIMILARITY.
 FT DISULFID 484 500 BY SIMILARITY.
 FT DISULFID 499 510 BY SIMILARITY.
 FT DISULFID 537 582 BY SIMILARITY.
 FT DISULFID 581 590 BY SIMILARITY.
 FT CONFLICT 503 503 S -> L (IN REF. 3).
 FT CONFLICT 531 531 H -> D (IN REF. 3).
 SQ SEQUENCE 607 AA; 70382 MW; 592BA417A36B66B CRC64;

Query Match 9.6%; Score 82; DB 1; Length 607;
 Best Local Similarity 24.2%; Pred. No. 3.5; Mismatches 19; Indels 50; Gaps 6;

44 DIVDQKNTVNDLVEF-----LPADVETNCESAFSCF---OKAQLKSAN 88
 DB 72 EINDFAKSCINDKTPCEKPVGTLEFDKLCADPAVGVNEMSECCARODPERAOCFKAH 131
 QY 89 TGNNERII---NVSITKILRK-----PSTNNGRQKHRLTQPS 124
 DB 132 ROHEHTSIRPEPEETCKLKEHPDDLISAFIEBARNHEDLYPAVALTKOYHKLAEHC 191
 QY 125 CDSYEKKPKPEFLERKSLQKMIHQHLSRTGSED 161
 DB 192 CEDEKKE--KCFSEKMKOLMK-----OSHIED 217

RESULT 9
 IL15_PIG 9
 ID IL15_PIG STANDARD; PRT; 162 AA.
 AC Q95253;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 TISSUE=Blood;
 MEDLINE=97449311; PubMed=9305780;
 RA Canals A., Grimm D.R., Gasparre L.C., Lunney J.K., Zarlenga D.S.;
 RT Molecular cloning of cDNA encoding porcine interleukin-15.*;
 RL Gene 195:337-339(1997).

CC -I- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: BELONGS TO THE IL-15 FAMILY.

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DR EMBL: U58142; AAB72031.1; -
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15; 1.
 KW cytokine; glycoprotein; signal.

FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 48 POTENTIAL.
 FT CHAIN 49 162 INTERLEUKIN-15.
 FT DISULFID 83 133 POTENTIAL.
 FT DISULFID 90 136 POTENTIAL.
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 162 AA; 18437 MW; 7EF792391883446 CRC64;

Query Match 9.5%; Score 80.5; DB 1; Length 162;
 Best Local Similarity 24.2%; Pred. No. 1.1; Mismatches 20; Indels 27; Gaps 6;

QY 45 IVDQKNTVNDLVEF-----LPADVETNCESAFSCF---OKAQLKSANTG 90
 DB 53 VISDLK-IEDLRISMDATLYTESDAHPNCKVTFAMKCFLELRVILQESRNSDISDTV 111
 QY 91 NNERII-NVSITKILRKRPSTNNGRQKHRLTQPS CDSYEKKPKPEFLERKSLQKMIH 149
 DB 112 ENLILANSSLSIEYK--TESG-----CKECELBEKKNINEFLKSFTHIVOMFTIN 160

RESULT 10
 YIM7_YEAST
 ID YIM7_YEAST STANDARD; PRT; 206 AA.
 AC P40470;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypoetical 23.8 kDa protein in MERT18-STY1 intergenic region.
 GN YIL127C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RA Barrett B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
 RA Louis E., Iye G., Moule S., Moule T., Odell C., Pearson D.,
 RA Rajandream M.A., Riles L., Kowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

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DR EMBL: Z46833; CAA86865.1; -
 DR SGD: S0001389; YIL127C.
 KW Hypothetical protein.
 SQ SEQUENCE 206 AA; 23845 MW; 4E51B11216F7ECB8 CRC64;

Query Match 9.3%; Score 79; DB 1; Length 206;
 Best Local Similarity 26.1%; Pred. No. 1.9; Mismatches 46; Indels 16; Gaps 3;

QY 48 QLNKNTVNDLVEFLPAPDEVETNCESAFSCFQKQLKSANTGNNERIINVSITKILRKRP 107
 DB 12 QATSVNGVGLSLNLDLPGPKIRANGKTSVNGSKQLIDRNLRKRYQLODRVHRIKKKC 71
 QY 108 PSTNNGRQKHRLTQPS CDSYEKKPKPEFLER--KSLQKMIHQHLSRT 156
 DB 72 KLVKKKKVKKHKL-----DKEDLEQALAKHQVLK--HDEGTLT 108

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GN KNSLS OR MKLPI.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024924; PubMed=1406973;
RA Nislow C., Lombillo V.A., Kuriyama R., McIntosh J.R.;
RT "A plus-end-directed motor enzyme that moves antiparallel
RT microtubules in vitro localizes to the interzone of mitotic
RT spindles."
RL Nature 359:543-547(1992).
RN [2]
RP REVISIONS.
RA Gryka M.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLUS-END-DIRECTED MOTOR ENZYME THAT MOVES ANTIPARALLEL
CC MICROTUBULES IN VITRO. LOCALIZES TO THE INTERZONE OF MITOTIC
CC SPINDLES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X67155; CAA47628.2; -.
DR PIR; S28262; S28262.
DR HSSP; P33176; 1BQ2.
DR MIM; 605064; -.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM004129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR Motor protein; Cell division; Microtubules; ATP-binding; Coiled coil;
DR Mitosis; Cell cycle; Nuclear protein.
FT DOMAIN 1 352 KINESIN-MOTOR.
FT DOMAIN 535 620 COILED COIL (POTENTIAL).
FT DOMAIN 7 11 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT NP BIND 112 119 ATP (BY SIMILARITY).
SO SEQUENCE 856 AA; 98105 MW; DDE7CEB480ABE58A CRC64;

Query Match 9.1%; Score 77; DB 1; Length 856;
Best Local Similarity 22.9%; Pred. No. 15;
Matches 44; Conservative 32; Mismatches 70; Indels 46; Gaps 10;

OY 1 MRSPGNMERIVCLWVIF--EGTL-----VHKSSSGSGDHRMIRMLDIYDLQKNVY 53
    ||| : || : || : || : || : || : || : || : || : || : || : || :
DB 122 MTGSPGEGGLPCPLDITNIGSGFOARKYFFKSN-----DRNSMDIOCEVDAL--LEQRK 175

OY 54 NDIVP-----EFLPAPDEVETNCWMAFSCFOKAQLKSANTGN 91
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 176 REAMPNPKTSSSKROYDPPEFADMITVOEFCKA--EEVEDGSYGVGFVSY----TEIYNNYI 230

OY 92 NERLINVSIKKLKRKPSTNNAQRKQ--RLTLCPSGDSDEKKKPPREFLEPR--KSLQKKMI 148
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 231 YDLLEEVPEPDLPKPKPOSKLLREDKNNMYVAGCTEVEYKSTEEAFEFWRGQKKRRIA 290

OY 149 HOHL---SSRTH 157
    : || ||| :
DB 291 NTHLNRESSRSKH 302

RESULT 13
INT3 DROME

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ID      VIT3_DROME      STANDARD:      PRT:      420 AA.
AC      P06607;
DT      01-JAN-1988 (Rel. 06, Created)
DR      01-JAN-1988 (Rel. 06, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Vitellogenin III precursor (Yolk protein 3).
GN      YP3.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CANTON-S.
RX      MEDLINE=87305580; PubMed=31114046;
RA      Garabedian M.J., Shiras A.D., Bownes M., Wensink P.C.;
RT      "The nucleotide sequence of the gene coding for Drosophila
RT      melanogaster yolk protein 3."
RL      Gene 55:1-8(1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=87146365; PubMed=3029679;
RA      Yan Y.L., Kunert C.J., Postlethwait J.H.;
RT      "Sequence homologies among the three yolk polypeptide (Yp) genes in
RT      Drosophila melanogaster."
RL      Nucleic Acids Res. 15:67-68(1987).
[3]
SEQUENCE FROM N.A. (MUTANT YP3S1).
MEDLINE=91360094; PubMed=1909425;
RA      Liddell S., Bownes M.;
RT      "Characterization, molecular cloning and sequencing of YP3s1, a
RT      fertile yolk protein 3 mutant in Drosophila."
RL      Mol. Gen. Genet. 228:81-88(1991).
[4]
FUNCTION: VITELLOGENIN IS THE MAJOR YOLK PROTEIN OF EGGS WHERE
IT IS USED AS A FOOD SOURCE DURING EMBRYOGENESIS.
[5]
TISSUE SPECIFICITY: SYNTHESIZED IN THE FAT BODY AND OVARIAN
FOLLICLE CELLS AND ACCUMULATE IN THE OOCYTE.
[6]
INDUCTION: By beta-ecdysone; in males.
[7]
MISCELLANEOUS: THE MUTANT YP3-S1 IS SYNTHESIZED IN THE FAT BODY,
BUT NOT SECRETED, PROBABLY DUE TO THE AMINO ACID MUTATION IN THE
SIGNAL PEPTIDE.
[8]
SIMILARITY: PARTIAL, TO LIPASES. STRONG TO OTHER VITELLOGENINS.
[9]
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DR      EMBL: M15898; AAA29024.1; -.
DR      EMBL: X04754; CAA28451.1; -.
DR      PIR: A27388; A27388.
DR      PIR: A25876; A25876.
DR      Flybase: FBgn0004047; YP3.
DR      InterPro: IPR000734; Lipase.
DR      Pfam: PF00151; Lipase; 1.
KW      Yolk; Signal.
FT      SIGNAL      1      19
FT      CHAIN      20      420      VITELLOGENIN III.
FT      VARIANT      10      10      A -> D (IN MUTANT YP3S1).
SQ      SEQUENCE      420 AA; 46101 MW; 5457C49CAC933B26 CRC64;

Query Match      9.0%; Score 76.5; DB 1; Length 420;
Best Local Similarity 24.4%; Pred. No. 7.4;
Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;
OY      8 MERIVICLVWIFGLVHSSSGODR-----HMIRKROLIDI----- 45
DB      1 MMSLRICLATCLVAHAHSAKSDANDRLKPTKWTATLETENPVLNDITWERTLENPLEQ 60

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OY      46 -----VDOLKNVNDLVEPLPAPEDVEFTNCWSAFSCFOKAOLK-----SA 87
DB      61 GAKYIEIYVGOIK---HDLTPSEVPSPSNVY---WIKSGQAVECKINNYETATA 114
OY      88 NTGNNERIINVSIRKL-KRKPSTNAGR-----QKHRL 120
DB      115 QPGGEDEVITVLGPKTSPAQOKAMRRLIQAVQKYNL 154

RESULT 14
ID      YG3M_YEAST      STANDARD:      PRT:      864 AA.
AC      P48237;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical 101.4 kDa protein in RPL4B-RSRL intergenic region.
GN      YGR150C OR G6642.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=5288C;
RX      MEDLINE=96158062; PubMed=8585325;
RA      Skala J., Nawrocki A., Goffeau A.;
RT      "The sequence of a 27 kb segment on the right arm of chromosome VII
RT      from Saccharomyces cerevisiae reveals MOLI, NAT2, RPL30B, RSRL, CY54,
RT      PEM1/CHO2, NSRL genes and ten new open reading frames."
RL      Yeast 11:1421-1427(1995).
[2]
SIMILARITY: SOME, TO S.POMBE SPBC1967.07C.
[3]
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DR      EMBL: X85807; CAA59808.1; -.
DR      EMBL: Z72935; CAA97164.1; -.
DR      SGD: S0003362; YGR150C.
DR      InterPro: IPR002885; PPR.
DR      Pfam: PF01535; PPR; 1.
KW      Hypothetical protein.
SQ      SEQUENCE      864 AA; 101422 MW; 5A773DEAA33D84FE CRC64;

Query Match      9.0%; Score 76.5; DB 1; Length 864;
Best Local Similarity 22.5%; Pred. No. 17;
Matches 43; Conservative 22; Mismatches 59; Indels 67; Gaps 8;
OY      2 RSSPGNMRIVIC---LMVIFLGLTVHKSSSQGDHMIIRMLQIDIVOLKNVNDLV 57
DB      5 RCGPKNN---VLCPFPOLSFLESKRLINK-----RFKTYLTQTEDE-KNMGSLS 49
OY      58 PEPLPAPEDVEFTNCWSAFSCFOKAOLKSANTGNNERIINVSIRKLKRKPSTNAGROR 117
DB      50 KNKITTPEDEV-----FKLAQLREFSNTLKERIHNTK-----SVNSDGHQS 90
OY      118 HRLTCPCSDYEKKPPK-----EFLERFSLLQKMTHQ----- 150
DB      91 NSIAPISDSRNANVTJTSVNPNEKSKNLSDLIHSFLEKMDLVPKYIRERVAADDIL 150
OY      151 --HLSRTHGS 159
DB      151 AKNLFDRSHSN 161

RESULT 15

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ALLA_YEAST
ID ALLA_YEAST STANDARD: PRT; 195 AA.
AC P32459;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ureidoglycolate hydrolase (EC 3.5.3.19).
GN DAL3 OR YIR032C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92133160; PubMed=1776360;
RA Yoo H.S., Cooper T.G.;
RT "The ureidoglycolate hydrolase (DAL3) gene in Saccharomyces
RT cerevisiae."
RT Yeast 7:693-698(1991).
(2)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Hornell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lyle G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UTILIZATION OF PURINES AS SECONDARY NITROGEN SOURCES,
CC WHEN PRIMARY SOURCES ARE LIMITING.
CC -1- CATALYTIC ACTIVITY: (-)-ureidoglycolate + H(2)O = glyoxylate + 2
CC NH(3) + CO(2).
CC -1- PATHWAY: THIRD STEP IN THE DEGRADATION OF ATLANTOIN (PURINE
CC CATABOLISM).
CC -----
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CC -----
DR EMBL; M64778; AAA73025.1; -
DR EMBL; Z38061; CAA86192.1; -
DR PIR; S42022; S42022.
DR PIR; S48494; S48494.
DR SCD; S0001471; DAL3.
KW Hydrolase; Purine metabolism; Prenylation; Lipoprotein.
FT LIPID 192 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 195 AA; 21727 MW; 6230AEB69585206B CRC64;

```

Query Match 8.9%; Score 76; DB 1; Length 195;
 Best Local Similarity 27.6%; Pred. No. 3.4; Mismatches 29; Indels 20; Gaps 3;
 Matches 24; Conservative 14;

```

OY 24 VHKSSGQDRHMRKQLDIVDOLKNTVNDVPEFLPAPEDVETNCWSAFSCFOKAQ 83
OY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 33 LEKGANGT---AIKLLQ-----VSQVENKSTKVP-----NMNLFRCFPDPH 72
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 84 LKSANTGNERRINVSIRKIKRRKPPST 110
OY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 73 LNRVFTGSGNQAIASHISIKVLEKHPGST 99
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: June 28, 2002, 07:43:22
 Job time: 157 sec

